

BLASTN 2.2.19+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: URU2TF3R016

Database: All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

8,293,739 sequences; 26,430,693,440 total letters

Query= SID_3

Length=2660

Sequences producing significant alignments:		Score (Bits)	E Value
gb K00470.1 HUMGHV	Homo sapiens growth hormone variant precur...	4913	0.0
gb J03071.1 HUMGHCS	Human growth hormone (GH-1 and GH-2) and...	4831	0.0
gb AC040958.20	Homo sapiens chromosome 17, clone RP11-630H24...	4806	0.0
gb EU421715.1	Homo sapiens growth hormone 2 precursor (GH2) ...	3949	0.0
gb AC127029.12	Homo sapiens chromosome 17, clone CTC-264K15...	3864	0.0
gb M13438.1 HUMGHN	Human growth hormone gene (HGH-N), complet...	3795	0.0
gb AC198149.2	Nomascus leucogenys BAC clone CH271-32K4 from ...	3413	0.0
emb C1954302.6	N.leucogenys DNA sequence from clone CH271-26...	3402	0.0
gb EU421712.1	Homo sapiens growth hormone 1 (GH1) gene, comp...	3254	0.0
gb AF374233.1	Pan troglodytes growth hormone (GH-V) gene, co...	3236	0.0
gb DQ002799.1	Macaca mulatta growth hormone 1 (GH-1), chorio...	3179	0.0
gb AC203687.3	MACACA MULATTA BAC clone CH250-171J17 from chr...	3072	0.0
gb AC015651.18 AC015651	Homo sapiens chromosome 17, clone RP1...	2957	0.0
gb K02401.1 HUMCS1	Human chorionic somatomammotropin gene hCS...	2950	0.0
gb M15895.1 HUMCS5	Human chorionic somatomammotropin CS-5 pse...	2929	0.0
gb J00289.1 HUMPLA	Homo sapiens placental lactogen hormone pr...	2909	0.0
gb M15894.1 HUMCS3	Human chorionic somatomammotropin hCS-3 gene	2852	0.0
gb EU421714.1	Homo sapiens chorionic somatomammotropin hormo...	2811	0.0
gb EU421716.1	Homo sapiens chorionic somatomammotropin hormo...	2787	0.0
emb V00520.1	Human germ line gene for growth hormone (presom...	2784	0.0
gb EU421713.1	Homo sapiens chorionic somatomammotropin hormo...	2767	0.0
gb AF374232.1	Pan troglodytes growth hormone (GH-N) gene, co...	2741	0.0
gb AY146625.1	Pan troglodytes placental lactogen PL-A gene, ...	2689	0.0
gb AY146626.1	Pan troglodytes placental lactogen PL-B gene, ...	2507	0.0
gb DQ002803.1	Macaca mulatta chorionic somatomammotropin hor...	2440	0.0
gb AY146628.1	Pan troglodytes placental lactogen PL-D gene, ...	2411	0.0
gb U02293.1 MMU02293	Macaca mulatta growth hormone-variant ge...	2331	0.0
emb AM235212.1	Callithrix jacchus gh (growth hormone) gene r...	2272	0.0
gb AY146627.1	Pan troglodytes placental lactogen PL-C gene, ...	2263	0.0
emb AM235213.1	Cebus albifrons gh gene for growth hormone pr...	2233	0.0
emb AM260481.1	Cebus albifrons growth hormone like pseudogene 6	2226	0.0
gb AF285183.1 AF285183	Cloning vector pSGHV0, complete sequence	2217	0.0
gb AY621641.1	Nomascus leucogenys growth hormone-like protei...	2198	0.0
emb CR610932.1	full-length cDNA clone CS0DI030YP11 of Placen...	2170	0.0
emb CR595678.1	full-length cDNA clone CS0DI030YK15 of Placen...	2165	0.0
emb AM260482.1	Cebus albifrons growth hormone like pseudogene 7	2141	0.0
emb CR614095.1	full-length cDNA clone CS0DI083YB03 of Placen...	2130	0.0
gb AY621637.1	Nomascus leucogenys growth hormone-like protei...	2119	0.0
emb CR601644.1	full-length cDNA clone CS0DI053YA22 of Placen...	2111	0.0
gb AY621636.1	Nomascus leucogenys growth hormone-like protei...	2108	0.0
emb AM260483.1	Cebus albifrons growth hormone like pseudogene 8	2098	0.0

gb AY744456.1	Callicebus moloch growth hormone-like protein ...	2084	0.0
emb CR607774.1	full-length cDNA clone CS0DI076YA16 of Placen...	2045	0.0
gb AF374234.1	Ateles geoffroyi growth hormone (GH-N) gene, c...	2036	0.0
gb AY744451.1	Alouatta seniculus growth hormone-like protein...	2028	0.0
gb AY744453.1	Alouatta seniculus growth hormone-like protein...	2015	0.0
gb AY744459.1	Callicebus moloch growth hormone-like protein ...	2012	0.0
gb AY621647.1	Pygathrix roxellana growth hormone-like protei...	2002	0.0
gb AY744458.1	Callicebus moloch growth hormone-like protein ...	1980	0.0
gb AY621645.1	Pygathrix nemaeus growth hormone-like protein ...	1978	0.0
emb AJ489811.1	CJA489811 Callithrix jacchus ghlp6 gene for gr...	1978	0.0
gb AY621643.1	Pygathrix nemaeus growth hormone-like protein ...	1975	0.0
emb AM260485.1	Cebus albifrons growth hormone like pseudogene 5	1925	0.0
gb DQ002802.1	Macaca mulatta chorionic somatomammotropin hor...	1925	0.0
gb AY744452.1	Alouatta seniculus growth hormone-like protein...	1901	0.0
gb AY744464.1	Pithecia pithecia growth hormone-like protein ...	1881	0.0
gb AY744462.1	Pithecia pithecia growth hormone-like protein ...	1877	0.0
gb AF374235.1	Ateles geoffroyi growth hormone (GH-V) gene, c...	1855	0.0
gb AY744457.1	Callicebus moloch growth hormone-like protein ...	1849	0.0
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gb AY744463.1	Pithecia pithecia growth hormone-like protein ...	1845	0.0
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gb AY744454.1	Alouatta seniculus growth hormone-like protein...	1821	0.0
gb AY621638.1	Nomascus leucogenys growth hormone-like protei...	1783	0.0
gb AY621640.1	Nomascus leucogenys growth hormone-like protei...	1770	0.0
gb AY621635.1	Hylobates leucogenys growth hormone-like 1 (gh...	1770	0.0
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gb AY744460.1	Callicebus moloch growth hormone-like protein ...	1751	0.0
gb AY621644.1	Pygathrix nemaeus growth hormone-like 3 (ghlp3...	1742	0.0
emb AJ489807.1	CJA489807 Callithrix jacchus ghlp2 pseudogene	1720	0.0
gb AY621653.1	Macaca assamensis growth hormone-like 3 (ghlp3...	1711	0.0
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gb AY744461.1	Pithecia pithecia growth hormone-like protein ...	1692	0.0
gb AY621651.1	Macaca assamensis growth hormone-like protein ...	1674	0.0
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gb AY621648.1	Pygathrix roxellana growth hormone-like protei...	1657	0.0
emb AJ489810.1	CJA489810 Callithrix jacchus ghlp5 gene for gr...	1657	0.0
gb AY621646.1	Pygathrix nemaeus growth hormone-like protein ...	1653	0.0
gb AY621642.1	Pygathrix nemaeus growth hormone-like protein ...	1653	0.0
gb AY744455.1	Alouatta seniculus growth hormone-like protein...	1640	0.0
gb AY621654.1	Macaca assamensis growth hormone-like protein ...	1622	0.0
gb AY621650.1	Pygathrix roxellana growth hormone-like protei...	1611	0.0
gb AY621655.1	Macaca assamensis growth hormone-like protein ...	1581	0.0
gb AY435434.1	Ateles geoffroyi GH-C gene, partial cds	1541	0.0
ref NM_022557.2	Homo sapiens growth hormone 2 (GH2), transcr...	1319	0.0
gb J03756.1	HUMGHVA Human growth hormone-variant (GH1) and gr...	1308	0.0
emb CR621109.1	full-length cDNA clone CS0DI055YC07 of Placen...	1297	0.0
emb CR594288.1	full-length cDNA clone CS0DI039Y013 of Placen...	1221	0.0
ref XM_001156416.1	PREDICTED: Pan troglodytes similar to gro...	1127	0.0
ref XM_001156130.1	PREDICTED: Pan troglodytes similar to gro...	1105	0.0
emb CR603719.1	full-length cDNA clone CS0DI042YM19 of Placen...	1096	0.0
emb CR624740.1	full-length cDNA clone CS0DI069YK20 of Placen...	1051	0.0
emb CR592007.1	full-length cDNA clone CS0DI026YA17 of Placen...	1046	0.0
emb CR590740.1	full-length cDNA clone CS0DI024YB06 of Placen...	1046	0.0
ref NM_022640.2	Homo sapiens chorionic somatomammotropin hor...	1040	0.0
emb CR618773.1	full-length cDNA clone CS0DI027YA22 of Placen...	1038	0.0
emb CR590972.1	full-length cDNA clone CS0DI009YJ04 of Placen...	1038	0.0
emb CR619097.1	full-length cDNA clone CS0DI049YD11 of Placen...	1037	0.0
emb CR612411.1	full-length cDNA clone CS0DI081YA23 of Placen...	1031	0.0

ALIGNMENTS

>gb|K00470.1|HUMGHV Homo sapiens growth hormone variant precursor (GH-V) gene, compl
 cds
 Length=2660

Score = 4913 bits (2660), Expect = 0.0
 Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
 Strand=Plus/Plus

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Sbjct 1      GAATTCAGCAGCTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60

Query 61     TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
            |||
Sbjct 61     TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120

Query 121    GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
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Sbjct 121    GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180

Query 181    TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACGTGACCC 240
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Sbjct 181    TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACGTGACCC 240

Query 241    TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTCACA 300
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Sbjct 241    TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTCACA 300

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Sbjct 301    CGCTGGTGATGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG 360

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Sbjct 421    CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCAC 480

Query 481    AAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGGAC 540
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Sbjct 481    AAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGGAC 540

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Query 601    CCTGAGGGGAGAGGCGCGTCTCTAGATGGGACGGGGGCACTAACCTCAGGTTTGGGG 660
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Sbjct 661    CTTATGAATGTTAGCTATCGCCATCTAAGCCAGTATTGGCCCAATCTCTGAATGTTCT 720

Query 721    GGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
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Sbjct 721    GGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
  
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Query	781	GAGAGCGCTGGCCCTCTTGCTCTCCAGCTCCCTCTGTTGCCTCCGGTTTCTCCCCAGGCTC	840
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Sbjct	841	CCGGACGTCCCTGCTCCTGGCTTTTGGCTGCTCTGCCTGTCTGGCTTCAAGAGGGCAG	900
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Sbjct	901	TGCCTTCCCAACCAITCCCTTATCCAGGCTTTTTTGACAACGCTATGCTCCGCGCCCGTCTG	960
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Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAGACTA	1080
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Query	1381	CCCGGGCAGCAGCAGCACTGCCGGTCCTTCCCTGCAGAACCTAGAGCTGCTCCGCATCT	1440
Sbjct	1381	CCCGGGCAGCAGCAGCACTGCCGGTCCTTCCCTGCAGAACCTAGAGCTGCTCCGCATCT	1440
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Sbjct	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCTCAGGAGCGCTTTCGCCA	1500
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Query	1561	AAGGCATCCAAACCGTGATGTGGGTGAGGGTGGCACCAGGATCCAATCTGGGGCCCCAC	1620
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Query   2581  AGCCAGTITGGACATTGAGTTGTTTGGCTTGGCACTGTCCTCTCATGCATTGGGTCCACTC  2640
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Query   2641  AGTAGATGCTTGTGAATTC  2660
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Sbjct   2641  AGTAGATGCTTGTGAATTC  2660

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>gb|J03071.1|HUMGHCSA Human growth hormone (GH-1 and GH-2) and chorionic somatomammone (CS-1, CS-2 and CS-5) genes, complete cds
Length=66495

Score = 4831 bits (2616), Expect = 0.0
Identities = 2652/2667 (99%), Gaps = 12/2667 (0%)
Strand=Plus/Plus

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Query   361      GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG  420
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Sbjct   41946  GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG  42005

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Query   481      AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTCTGTGGAC  540
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Query   599      GTCCTGAGGGGAGAGGCGGCTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG  658
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Sbjct	42186	GTCTTGAGGGGAGAGGCGCGTCTGTAGATGGGACGGGGGCTAACCCTCAGGTTTGG	42245
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Sbjct	42305	CTGGTCCCTGAGAGGAGGAGAGAGAGAGAGAGAGAAAAAAACCAGCTCCTGGAAC	42364
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Sbjct	42725	GAGGTTCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGTC	42784
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Sbjct	43025	TCTCCTCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTTCG	43084
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Sbjct	43085	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCGCCACCTGAAGGACCTAG	43144
Query	1558	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC-AATCCTGGGGC	1615
Sbjct	43145	AGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCCAATCCTGGGGC	43204
Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTCAGTCAGTCAGGC	1675
Sbjct	43205	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTCAGTCAGTCAGGC	43264
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Sbjct	43265	GCTGACCCAAGAGAACTACCGTATTCTTCAATTTCCCTCGTGAATCCTCCAGGCCCTTC	43324
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Sbjct	43325	TCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCC	43384
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Sbjct	43385	AAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCCCC	43444
Query	1856	GGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAACGATG	1915
Sbjct	43445	GGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAAATCGCACAAACGATG	43504
Query	1916	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTGCG	1975
Sbjct	43505	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTGCG	43564
Query	1976	AGACATTCCTGCGCATCGTGCAAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	2035
Sbjct	43565	AGACATTCCTGCGCATCGTGCAAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	43624
Query	2036	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCCTGGTCGTGGAAGGTGCTACTC	2095
Sbjct	43625	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCCTGGTCGTGGAAGGTGCTACTC	43684
Query	2096	CAGTGCCCAACAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTITGACTAGGTGT	2155
Sbjct	43685	CAGTGCCCAACAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTITGACTAGGTGT	43744
Query	2156	CCTTGATAAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCAGGTTGGGAAG	2215
Sbjct	43745	CCTTGATAAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAAG	43803
Query	2216	ACAACCTGTAGGGCCCTTCAGGGTCTATTTCGGGAACAGGGCTGGAGTGCAGTGGCA-G-TC	2273
Sbjct	43804	ACAACCTGTAGGGCCCTTCAGGGTCTATT-TGGGAACAGGGCTGGAGTGCAGTGGCACGATC	43862
Query	2274	TTGGCTCGCTGCAATCTCCGCCTCTGGGTTCAAGCGATTCTCTGCCCTCAGTCTCCCGA	2333
Sbjct	43863	TTGGCTCGCTGCAATCTCCGCCTCTGGGTTCAAGCGATTCTCTGCCCTCAGTCTCCCGA	43922
Query	2334	ATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTAGAG	2393
Sbjct	43923	ATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTAGAG	43982
Query	2394	ACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCCC	2453


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Sbjct  43983  ACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC  44042
Query  2454    GCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCCT  2513
          |||
Sbjct  44043  GCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCCT  44102
Query  2514    GTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGC  2573
          |||
Sbjct  44103  GTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGC  44162
Query  2574    CATGCCAGCCAGTTGGACATTGAGTTGTTGCTTGGCACTGTCCTCTCATGCATTGGG  2633
          |||
Sbjct  44163  CATGCCAGCCAGTTGGACATTGAGTTGTTGCTTGGCACTGTCCTCTCATGCATTGGG  44222
Query  2634    TCCACTCAGTAGATGCTTGTGAAATC  2660
          |||
Sbjct  44223  TCCACTCAGTAGATGCTTGTGAAATC  44249

Score = 3886 bits (2104), Expect = 0.0
Identities = 2491/2675 (93%), Gaps = 38/2675 (1%)
Strand=Plus/Plus

Query  1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT  60
          |||
Sbjct  4671    GAATTCAGGACTGAATCGTGCTCACAACCCCAACAATCTATTGGCTGTGC-TTGGCCCT  4729
Query  61      TTTCCTCCAAACACACATTCTGTCTGGTGGGTGGAGGGGAAACATCGGGGAGGAGGAAAG  120
          |||
Sbjct  4730  TTTCCTCCAAACACACATTCTGTCTGGTGGGTGGAGGTTAAACATCGGGGAGGAGGAAAG  4789
Query  121     GAATAGGATAGAGAGTGGGATGGGGTCGGTA-GGGGTCTCAAGGACTGGCCTATCCTGAC  179
          |||
Sbjct  4790  GGATAGGATAGAGAAATGGGATGTGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGAC  4848
Query  180     ATCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACC  239
          |||
Sbjct  4849  ATCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCGGCCAGAGGGCACCCACGTGACC  4908
Query  240     CTTAAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATTCCTGTGCACAACCTCACA  299
          |||
Sbjct  4909  CTTAAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATCTCTGTGCACAACCTCACA  4968
Query  300     ACGCTGGTGATGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGT  359
          |||
Sbjct  4969  ACGCTGGTGACGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGT  5028
Query  360     GGGAGGAGCTTCTAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCCAGGCCATAACAT  419
          |||
Sbjct  5029  GGGAGGAGCTTCTAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCCATGCATAAAATGT  5088
Query  420     GCAGAGAAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAGGGCCC  478
          |||
Sbjct  5089  ACACAGAAAACAGGTG-GGGGCAA-CAGTGGGAGAGAGAAGGGGCCAGGTATAAAAGGGCCC  5146
Query  479     ACAAGAGACCAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTCTGTGG  538
          |||
Sbjct  5147  ACAAGAGACCAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTCTGTGG  5206
Query  539     ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCTAAAATCCCTTT-GGCACAAT  596

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Sbjct	5207	ACAGCTACACCTAGCGGCAATGGCTACAGGTAAAGCGCCCTAAAAATCCCTTTGGGCACAAT	5266
Query	597	GTGTCCTGAGGGGAGAGGCGCGCTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	656
Sbjct	5267	GTGTCCTGAGGGGAGAGGACGACCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	5326
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCGATATTGGCCCAATCTCTGAATGT	716
Sbjct	5327	GGGGCTTCTGAATGTGAG-TATCGCCATGTAAGCCCGATATTGGCCCAATCTCAGAAAGC	5385
Query	717	TCCTGGTCCCTGAGGAGGCGAGAGAGAGAGAGAGAAAAAAACCAGCTCCTGGAA	776
Sbjct	5386	TCCTGGTCCCT---GGA-G--G-GA-TG-GAGAGAG-AAAAACAA--CAGCTCCTGGAG	5433
Query	777	CAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTGG--CCTCCGGTTCTCCCCA	835
Sbjct	5434	CAGGGAGAGTGCTGGCCTCTTGCTCTCCGGCTCCCTCTGTGGCCTCTGGTTCTCCCCA	5493
Query	836	GGCTCCCGGAGCTCCCTGCTCTGGCTTTTGGCTGCTCTGCTGCTGCTGGCTTCAAGAG	895
Sbjct	5494	GGCTCCCGGAGCTCCCTGCTCTGGCTTTTGGCTGCTCTGCTGCTGCTGGCTTCAAGAG	5553
Query	896	GGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTGACACGCTATGCTCCGCGCC	955
Sbjct	5554	GGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTGACACGCTATGCTCCGCGCC	5613
Query	956	CGTCGCGTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATG	1015
Sbjct	5614	CATCGCTGCACACGCTGGCCTTGTGACACCTACCAGGAGTTTGTAAAGCTCTTGGGGAATG	5673
Query	1016	GGTGCCTTCAGAGGTGGCAGGAAGGGGTGAATTTCGCCCGCTGGGAAGTAATG--GGAGG	1074
Sbjct	5674	GGTGCCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCGCCCGCTGGGAAATAA--GAGGAGG	5732
Query	1075	AGACTAAGGAGCTCAGGGTTGTTTTCGAAAGTAAAAATGCAGGCAGATGAGCATACGCTG	1134
Sbjct	5733	AGACTAAGGAGCTCAGGGTT-TTCCCGAAGCGAAAAATGCAGGCAGATGAGCACACGCTG	5791
Query	1135	AGTGAGGTTCCCGAAAAAGTAACAATGGGAGCAGGTTCCAGCATAGACCTTGGTGGGCG	1194
Sbjct	5792	AGTGAGGTTCCCGAAAAAGTAACAATGGGAGCTGCTCCAGCGTAGACCTTGGTGGGCG	5851
Query	1195	GTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCTTCCTGCAGAA	1254
Sbjct	5852	GTCTTCTCCTAGGAAGAAGCCTATATCCCAAGGAAACAGAAGTATTCTTCCTGCAGAA	5911
Query	1255	CCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAAC	1314
Sbjct	5912	CCCCAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCTTCCAACAGGGAGGAAAC	5971
Query	1315	GCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGG--TGGGATGGGGTAGACCTGTGGT	1373
Sbjct	5972	ACAACAGAAATCCGTGAGTGGATGCCTTCTCCCAGGCGGGGATGGGGGAGACCTGTAGT	6031
Query	1374	CAGAGCCCCCGGCGAGCAGCAGCCACTGCCGGTCTTCCCTTGCAGAACCTAGAGCTGCTC	1433
Sbjct	6032	CAGAGCCCCCGGCGAGCAGCAGCAATGCCGCTCTTCCCTTGCAGAACCTAGAGCTGCTC	6091
Query	1434	CGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGAGCTCTCAGGAGCGTC	1493

Sbjct	6092		CGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCTCAGGAGTGTG	6151
Query	1494		TTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCG-CCACCTGAAGGA	1552
Sbjct	6152		TTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGCTCTAT-GACCTCCTAAAGGA	6210
Query	1553		CCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAC-CCATCC	1609
Sbjct	6211		CCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCC	6270
Query	1610		TGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGCTGCCCTCTTTTATGCA	1668
Sbjct	6271		TGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGCTGCCCTCTTTTATGCA	6329
Query	1669		GTCAGGCGTGACCCAAAGAGAACTACCGTATTCTTCAITTTCCCTCGTGAATCCTCCAG	1728
Sbjct	6330		GTCAGGCGTGACCCAAAGAGAACTACCTTATTCTTCAITTTCCCTCGTGAATCCTCCAG	6389
Query	1729		GCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGGAAC	1788
Sbjct	6390		GCCTTTCTCTACACCTGAAGGGGAGGGAGGAAATGAATGAATGAGAAAGGGAGGGGAAC	6449
Query	1789		AGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGACAGAGGTGGAAGATGGC	1848
Sbjct	6450		AGTACCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGACAGAGGTGGAAGATGGC	6509
Query	1849		AGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCAC	1908
Sbjct	6510		AGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTTGCACACAAACTCACAC	6569
Query	1909		AACGATGACGCACTGCTCAAGAAGTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	1968
Sbjct	6570		AACGATGACGCACTACTCAAGAAGTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	6629
Query	1969		AAGGTCGAGACATTCTCGCATCTGTCAGTGCCTCTGTGGAGGGCAGCTGTGGCTTC	2028
Sbjct	6630		AAGGTCGAGACATTCTCGCATCTGTCAGTGCCTCTGTGGAGGGCAGCTGTGGCTTC	6689
Query	2029		TAGTGTCCCGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGTCTGGAAGGT	2088
Sbjct	6690		TAGTGTCCCGGGTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGTCTGGAAGGT	6749
Query	2089		GCTACTCCAGTGCCACCAGCCITGTCTATAATAAATTAAGTGCATCATTTTGTCTGAC	2148
Sbjct	6750		GCCACTCCAGTGCCACCAGCCITGTCTATAATAAATTAAGTGCATCATTTTGTCTGAC	6809
Query	2149		TAGGTGTCTTGTATAATATTATGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGT	2208
Sbjct	6810		TAGGTGTCTTGTATAATATTATGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGT	6868
Query	2209		TGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACAGGCTGGAGTGCAGTGG	2268
Sbjct	6869		TGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACAGGCTGGAGTGCAGTGG	6928
Query	2269		CAG--TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAGCGATTCTCCTGCCTCAGT	2326
Sbjct	6929		CACAATCTTGGCTCAGTGCATCTCCGCCTCCTGGGTTCAGCGATTCTCCTGCCTCAGC	6988
Query	2327		CTCCCGAATAGTTCGAGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTT	2386

Sbjct	6989	 CTCCCCGAGTGTGGGATTCCAGGCATCGATGACCAGGCTCAGCTAATTTTTGTTTTC	7048
Query	2387	GGTAGAGACGGGGTTTACCATAATTGGCCAGTCTGGICTCCATCTCCTGACCTCAGGTAA	2446
Sbjct	7049	GGTAGAGACGGGGTTTACCATAATTGGCCAGGCTGGTCTCCAACCTCTTAATCTCAGGTGA	7108
Query	2447	TCCGCCCGCCTCGGCCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCC	2506
Sbjct	7109	TC TACCACCTTGGCCTCCCAAAT GCTGGGATTACAGCGTGAACCACTGCTCCCTTCC	7168
Query	2507	CTGTCTTG-TGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGC	2565
Sbjct	7169	 CTGTCTTCTGATTTTAAAATAACTATACCAGCAGGAGGACGTCCAGACACAGCATAGGC	7228
Query	2566	TACCTGGCCATGCCAGCCAGITGGACAATTGAGTGTGTTGCTTGGCACTGTCTCTCAT	2625
Sbjct	7229	 TACCTG-CCATGCCAACCGGTGGGACAATTGAGTGTGTTGCTTGGCACTGTCTCTCAT	7287
Query	2626	GCAITGGGTCCACTCAGTAGATGCTTGTGTAATTC	2660
Sbjct	7288	 GCGTIGGGTCCACTCAGTAGATG CCTGTGTAATTC	7322

Score = 2970 bits (1608), Expect = 0.0
Identities = 2071/2288 (90%), Gaps = 58/2288 (2%)
Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATCATGCCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCOCT	60
Sbjct	26916	 GAATTCAGGACTCAATGGTGCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCOCT	26974
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	26975	 TTTCCCAACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGGAGGAGGAAAG	27034
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCTTGACA	180
Sbjct	27035	 GAATAGGATAGAGAGTGGAAATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCTTGACA	27093
Query	181	TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCAGAGGGGCACCCAGTGACCC	240
Sbjct	27094	 GCCTTCCCGCGTTTCAGGTTGACCAACATGGCCTGCAGCCAGAGGGGCACCCACCTGACCC	27153
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTA-TCTCTGGCTGACATTCTGTGCACAACCCCTACA	299
Sbjct	27154	 TTAAAGAGAGGACAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGCACAATCCTTACA	27212
Query	300	ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT	359
Sbjct	27213	 ACACTGGTGATGGTGAGAAGGGAAAGACGACAAGCCAGGGGGCATGATCCCAGCATGTGT	27272
Query	360	GGGAGGAGCTTCTAAATATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACAT	419
Sbjct	27273	 GGGAGGAGCTTCTAAATATCCACTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	27332
Query	420	GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAGGGCCC	478
Sbjct	27333	 ACACAGAAACAGGTGGGGTCAAGCAGGGGAGAGAACTGGCCAGGGTATAAAAGGGGCC	27399

Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGG	538
Sbjct	27393	ACAAGAGACCGGCTCTAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGG	27452
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCTAAAAATCCCTTT-GGCACAAT	596
Sbjct	27453	ACAGCTCACCTAGTGGCAATGGCTGCCAGGTAAGCGCCCTAAAAATCCCTTTGGGCACAAC	27512
Query	597	GTGTCTCTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT	656
Sbjct	27513	GTGTCTCTGAGGGGAGAGGCGGCGTGTAGATGGGACGGGGGCACTAACCTCAGGTTT	27572
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG-TATTTGGCCAATCTCTGAATG	715
Sbjct	27573	GGGGCTTATGAATGTGAG-TATCGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATG	27631
Query	716	TTCTGGTCCCTGGGAGGAGGCAGAGAGAGAGAGAGAGAAAAAA-AAACCCAGCTCCTGG	774
Sbjct	27632	TTCTGGTCTCTGGA-G-GG-A-TG-GAGAGAGAGA-AAAAAACAAA--CAGCTCCTGG	27683
Query	775	AACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTG-CCTCCGGTTTCTCC	833
Sbjct	27684	AGCAGGGAGAGCGCTGGCCTCTTCTCTCCGGCTCCCTCCATIGCCCTCCGGTTTCTCC	27743
Query	834	CAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAG	893
Sbjct	27744	CAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAG	27803
Query	894	AGGGCAG-TGCCITCCCAACCATTCCTTATCCAGGCTTTTGTGACACGCTATGCTCCGC	952
Sbjct	27804	AGG-CTGCTGCCGTCCAAACCGTTCCGTTATCCAGGCTTTTGTGACACGCTATGCTCCAA	27862
Query	953	GCCCGTCGC-CTGIACCAGCTGGC-ATATGACACCTATCAGGAGTTTGAAGCTCTGGG	1010
Sbjct	27863	GCCCATCGCGC-GCACAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGTCTTGGG	27920
Query	1011	TAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGG	1070
Sbjct	27921	GAATGGGTGCGGCTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGAAGTAATGG	27980
Query	1071	GAGGAGACTAAGGAGCTCAGGTTGTTTTCTGAAGTGAAAAATGCAGGCAGATGAGCATA	1130
Sbjct	27981	GAGGAGACTAAGGAGCTCAGGTTGTTTTCTGAAGCGAAAAATGCAGGCAGATGAGCATAG	28040
Query	1131	GCTGAGTGAGGTTCCAGAAAAAGTAACAATGGGAGCAGGTTCCAGCATAGA--CC----	1184
Sbjct	28041	GCTGAGCCAGGTTCCAGAAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACCGCA	28100
Query	1185	-T--T----GGTGGGCGGTCCTTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAG	1237
Sbjct	28101	GTCTTCTTGTGGTGGGGGCTCTTCTCTAGGAAGAACTATATCCCAAAGGCAGAGAAG	28160
Query	1238	TATTCAATTCCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACC	1296
Sbjct	28161	TATTCAATTCCTGATGA-CTCCAGACCTCCTTCTGCTTCTCAGAGTCTATTCCGACACC	28219
Query	1297	TTCCAACAGGGTGAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCAAGGTGGG-	1355
Sbjct	28220	CTCCAACATGGAGGAAACGCACAGAAATCCGTGAGTGGATGCCGCTCCCTAGGCGGGG	28279

Query	1356	ATGGGGTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCCCTG	1415
Sbjct	28280	ATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGGTCTTCCCCCTG	28339
Query	1416	CAGAACCTAGAGCTGTCCGCATCTCCCTGTGCTCATCCAGTCAITGGCTGGAGCCCGTG	1475
Sbjct	28340	CAGAACTAGAGCTGTCCGCATCTCCCTGTGCTCATCGAGTCTGGCTGGAGCCCGTG	28399
Query	1476	CAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTC	1535
Sbjct	28400	CGTTTCCTCAGGAGTATGTTGCCAACAACTGGTGTATGACACCTCGGACAGCGATGAC	28459
Query	1536	TATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCA	1595
Sbjct	28460	TATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGCG	28519
Query	1596	CCAGGA-TC-C-AATCTGGGGCCCCACTGGCTTCAGGGACTGGGG-AGAGAAACACTG	1651
Sbjct	28520	CCAGGGGTACCAATCCTGGAACCCCACTGGCTTCGAGGG-CTGGGGGAGAGAAATACTG	28578
Query	1652	CTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCCGTAATCTTCAATTTC	1711
Sbjct	28579	CTGCCCTCTTTTAGCAGTAAGGCGCTGACCCAAGAGAACTACCTTATTCTTCAATTTCG	28638
Query	1712	CCTCGTGAATCCTCCAGGCCCTTCTCTACAACCTGGAGGGGAGGGAGGAAATGGATGAA	1771
Sbjct	28639	CCTGGTGAATCCTCCAGGCCCTTCTCTACAACCTGAAGGG-AGGGAGGAGGAAATGGATAAA	28697
Query	1772	TGAGAGAGGG-AGGGAACAGTGCCCAAGCGCTTGG-CCTCTCCTTCTCTCTTCACTTT	1829
Sbjct	28698	TGAGAGAGGGGAGGGAACAGTGCCCAAGCGCTTGACCTCTCCTTCTCTTCACTTT	28757
Query	1830	GCAGAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAA	1889
Sbjct	28758	GCAGAGGCTGGAAGAGCGCAGCCGCGACTGGGCAGATCCTCAAGCAGACCTACAGCAA	28817
Query	1890	GTTTGACACAAAAICGCACAACGATGACGCATGCTCAAGAACTACGGGCTGCTCTACTG	1949
Sbjct	28818	GTTTGACACAAACTCGCACAACCATGACGCATGCTCAAGAACTACGGGCTGCTCTACTG	28877
Query	1950	CTTCAGGAAGGACATGGACAAGGTCGAGACATCTCGCGCATCGTGCAGTGCCGCTCTGT	2009
Sbjct	28878	CTTCAGGAAGGACATGGACAAGGTCGAGACATCTCGCGCATGGTGCAGTGCCGCTCTGT	28937
Query	2010	GGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTIGIGACCCTCCCCAGTGCC	2069
Sbjct	28938	GGAGGGCAGCTGTGGCTTCTAGGTGCCCGAGTAGCATCC-TGTGACCCTCCCCAGTGCC	28996
Query	2070	TCTCTGGTCTGTGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAG	2129
Sbjct	28997	TCTCTGGCCCTG-AGGTTGCCACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAG	29055
Query	2130	TTGCATCATTTTGTGTTGACTAGGTGTCTTGATATAATATTATGGGGTGGG-GGCGGGTGG	2188
Sbjct	29056	TTGTATCATTTTCATCTGACTAGGTGTCAATTCTATAATATTATGGGGTGGGAGGTGG-TGG	29114
Query	2189	TATGGAGCAAGGGGCCAGGTGGGAAGACA-ACCTGTAGGGCCTTACGGGTCTATTTCGGG	2247
Sbjct	29115	TATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCGCTCAAGGTCTATT-TGG	29170

Query	776	ACAGGGAGAGCGCTGGCCCTCTTGCTCTCCAGCTCCCTCTGTG-CCTCCGGTTTCTCCCC	834
Sbjct	13015	ACAGGGAGAGTGCTGGCCCTCTTGCTCTGCGGCTCCCT-TCCTGCCCTCCGGTTTCTCCCC	13073
Query	835	AGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCTGTCTGGCTTCAAGA	894
Sbjct	13074	AGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCTGTCTGGCTTCAAGA	13133
Query	895	GGGC-AGTGCCTTCCCAACCAITCCCTTATCCAGGCTTTTGTACA-ACGCTATGCTCCGC	952
Sbjct	13134	-GGCTGGTGGCGTCCAAACCGTTCCTTATCCAGGCTTTT-AAAGAGGCTATGCTCCAA	13191
Query	953	GCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGG	1010
Sbjct	13192	GCCCATCGCGC-ACACCAGCTGGCCAT-TGACACCTACCAGGAGTTTATAAGCTCTTGGG	13249
Query	1011	TAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATG	1069
Sbjct	13250	GAATGGGTGCGGTTCAGGAGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGAAGTAATG	13309
Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTCTGAAGTAAAAATGCAGGCAGATGAGCATA	1129
Sbjct	13310	GGAGGAGACTAAGGAGCTCAGGGTTGTTTCTGAAGCAAAAATGCAGGCAGATGAGCATA	13369
Query	1130	CGCTGAGTGAAGTTCCAGAAAAGTAACAATGGGAGCAGGCTCCAGCAT---AG-A--	1182
Sbjct	13370	GGCTGAGCCAGGTTCAGAAAGAGTAACAGTGGGAGCTGGTCTCCAGCATAGAAAGCAGT	13429
Query	1183	---C--CTTGGTGGGCGGTCTTCTCTAGGAAGAAGCCTATATC-CTGAAGGAGCAGA	1235
Sbjct	13430	GGTCTCTCTTGGTGGGCGGTCTTCCCTAGGAAGAAGCCTATATCAC-AAAGGAACAGA	13488
Query	1236	AGTATTCATTCCTGCA-GAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATCCAA	1294
Sbjct	13489	AGTATTCATTCCTGCATG-ATCCCGAGACCTCCTTCTGCTTCTCAGACTCTATTTCGACA	13547
Query	1295	-CCTTCCAACAGGGTGAAAACGAGCAGAAATCTGTGAGTGGATGCC-TCTCCCCAGG-	1351
Sbjct	13548	TCC-TCCAACATGGAGAAACGAGCAGAAATCCGTGAGTGGATG-CTGTCT-CCTAGGC	13604
Query	1352	TGGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGAGCAGCCACTGCCGGTCTCTCC	1411
Sbjct	13605	GGGGATGGGGGAGACCTGTGGTCAGAGCCCCGGGAGCAGCCACTGCCGGTCTCTCC	13664
Query	1412	CTGCAAGAACCTAGAGCTGCTCCGATCTCCCTGTGCTCATCCAGTCTATGGCTGGAGCC	1471
Sbjct	13665	CCTGCAAGAACTAGAGCTGCTCCACATCTCCCTGTGCTCATCGAGTCTGGGCTGGAGCC	13724
Query	1472	CGTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGATGGCGCCTCGGACAGCAA	1531
Sbjct	13725	CGTGGCGTTCCTCAGGAGTACCTTCACCAACAACCTGGTGATGACACCTCGGACAGCGA	13784
Query	1532	CGTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGT	1591
Sbjct	13785	TGACTATCACCTCTTAAGGACCTAGAGGAAGGCATCCAAATGCTGATGGGGGTGAGGGT	13844
Query	1592	GGCACCAGGA-TCC--AATCTTGGG-GCCCCACTGGCTTCCAGGGACTGGGG-AGAGAAA	1646
Sbjct	13845	GGCACCAGGGTCCCCAATCTGGGAAGCCC-ACTGGCTTCGAGGG-CTGGGGGAGAGAAA	13902

Query 1647 CACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCCGTATTCTTCA 1706
 Sbjct 13903 CACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCCATATTCTTCA 13962

Query 1707 TTTCCTCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGAGGAAAATGG 1766
 Sbjct 13963 TTTCCTCCCTCGTGAATCCTCCAGGCCTTTCTCTACA-CCTGAAGGGGAGGAGGAAAATGG 14021

Query 1767 ATGAATGAGAGAGGGAGGGAACAGTCGCCAAGCGCTTGGCTCTCTCTCTCTCTCTCTAC 1826
 Sbjct 14022 ATAAATGAGAGAGGGAGGGAACAGTCGCCAAGCGCTTGGCTCTCTCTCTCTCTCTCTAC 14081

Query 1827 TTTCAGAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAG 1886
 Sbjct 14082 TTTCAGAGGCTGGAAGAGCGCAGCCACCTGACTGGGCAGACCTCAAGCAGACCTACAG 14141

Query 1887 CAAGTTTGACACAAAATCGCACACGATGACGCACCTGCTCAAGAACTACGGGCTGCTCTA 1946
 Sbjct 14142 CAAGTTTGACACAAATCGCACACCACTGACGCACCTGCTCAAGAACTACGGGCTGCTCCA 14201

Query 1947 CTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGAGTCGCCGCTC 2006
 Sbjct 14202 CTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGAGTCGCCGCTC 14261

Query 2007 TGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGT 2066
 Sbjct 14262 TGTGGAGGGCAGCTGTGGCTTCTAGGGGCCCGCGTGGCATCC-TGTGACCCCTCCCCAGT 14320

Query 2067 GCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGTCTTAATAAAAT 2126
 Sbjct 14321 GCCTCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCCAACAGCCTTGTCTTAATAAAAT 14379

Query 2127 AAGTTGCATCATTTTGTGTGACTAGGTGTCCTTGTATAATATTATGGGGTGA-GGCGGG 2185
 Sbjct 14380 AAGTTGTATTGTTTATCTGACTAGGTGTCCTTCTATAATATTATGGGGTGAAGGTGG- 14438

Query 2186 TGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTG 2245
 Sbjct 14439 TGGTATGGAGCAAGGGGT-AGGT-GGGAAGACGACCTGGAGGGCCTTCAGGGTCTATT-G 14495

Query 2246 GGAACCAAGC 2255
 Sbjct 14496 GGAACATAGC 14505

Score = 2920 bits (1581), Expect = 0.0
 Identities = 2065/2291 (90%), Gaps = 64/2291 (2%)
 Strand=Plus/Plus

Query 1 GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60
 Sbjct 49740 GAATTCAGCACTCAATGGTGTCTAGAACCCCAATCTATTGGCTGTGCT-TTGGCCCT 49798

Query 61 TTTCCTCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
 Sbjct 49799 TTTCCTCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACACGCGGGGAGGAGGAAAG 49858

Query 121 GAATAGGATAGAGAGTGGGATGGGGTCGTTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
 Sbjct 49858 GAATAGGATAGAGAGTGGGATGGGGTCGTTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180


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Sbjct  50744  AATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTG-ACCT-CCCCACTGGGGAAGTAATGG 50801
Query  1071    GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATAC 1130
          |||
Sbjct  50802  GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAATGCAGGCAGATGAGCATAG 50861
Query  1131    GCTGAGTGAGGTTCCAGAAAAAGTAACAATGGGAGCAGGCTCCAGCAT-----AG-A 1182
          |||
Sbjct  50862  GCTGAGCCAGGTTCCAGAAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACGACGA 50921
Query  1183    ---C---CTTGGTGGGCGGTCTTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAG 1237
          |
Sbjct  50922  GTCTTCTTGGTGGGCGGTCTTCTCTAGGAAGAAACCTATATCCCAAGGACCAGAAG 50981
Query  1238    TATTATTCTCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAAACACC 1296
          |||
Sbjct  50982  TATTATTCTCTGCATG-ACTCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACACC 51040
Query  1297    TTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCCTTCTCCCC-AGG-TGG 1354
          |||
Sbjct  51041  CTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGCTCTCCCTAGGCGGG 51100
Query  1355    GATGGGGTAGACCTGTGGTCAGAGCCCCCGGCGAGCACAGCCACTGCCGGTCCCTCCCT 1414
          |||
Sbjct  51101  GATGGGGGAGACCTGTGGTCAGGGCTCCCGGCGAGCACAGCCACTGCCGGTCCCTCCCT 51160
Query  1415    GCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTTCATGGCTGGAGCCCGT 1474
          |||
Sbjct  51161  GCAGAACTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCGT 51220
Query  1475    GCAGCTCTCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGT 1534
          |||
Sbjct  51221  GCGGTCTCTCAGGAGTATGTTGCCAACAACTGGTGTATGACACCTCGGACAGCGATGA 51280
Query  1535    CTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGC 1594
          |||
Sbjct  51281  CTATCACCTCTCTAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGTGAGGGTGGC 51340
Query  1595    ACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACACT 1650
          |||
Sbjct  51341  GCCAGGGGTGCGCAATCTTGGAAACCCACTGGCTTAGAGGG-CTGGGGGAGAGAAACA-T 51398
Query  1651    GCTGCCCTCTTTTATGAGTCAAGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTC 1710
          |||
Sbjct  51399  GCTGCCCTCTTTTATGAGTCAAGCGCTGACCCAAGAGAACTACCTTATTCTTCATTTC 51458
Query  1711    CCCTCGTGAATCTCCAGGCCCTTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGA 1770
          |||
Sbjct  51459  GCCTGCT-AATCCTCAGGCCCTTCTCTACAACCTGAAGGGGAGGGAGGAAAAATGGATGA 51517
Query  1771    ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCTCTCTCCTTTCACITTG 1830
          |||
Sbjct  51518  ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCTCTCTCCTTTCACITTG 51577
Query  1831    CAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAG 1890
          |||
Sbjct  51578  CAGAGGCTGGAAGACGGCAGCCCGGACTGGGCAGATCCTCAAGCAGACCTACAGCAAG 51637
Query  1891    TTTGACACAAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC 1950
          |||

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Sbjct  51638  TTTGACACAACTCACACAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC  51697
Query  1951    TTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGC CGCTCTGTG
|||||
Sbjct  51698  TTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATGTTGCAGTGC CGCTCTGTGTA
51757
Query  2011    GAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACC--CC--TCCCCAGT
|||||
Sbjct  51758  GAGGGTAGCTGTGGCTTCTAGGTGCCCGCGTGGCATCC-TGTGACCGACCCCTCCCCAGT
51816
Query  2067    GCCTCTCCTGGTCTGTGGAAGGTGCTACTCCAGTGGCCACCAGCCTTGTCTTAATAAAAATT
|||||
Sbjct  51817  GCCTCTCCTGGCCCTGGAAGGTGCCACTCCAGTGGCCATCAGCCTTGTCTTAATAAAAATT
51876
Query  2127    AAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATG GGGTGGGA-GGCGGG
|||||
Sbjct  51877  AAGTTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATG GGGTGGGAAGGTGG-
51935
Query  2186    TGGTATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCTATTTC
|||||
Sbjct  51936  TGGTATGGAGCAAGGGGGT-AGGT-GGAAAGA-AGACCTGAGGGGCCTTCAAGATCTATT-
51991
Query  2245    GGGAAACAGGC 2255
|||||
Sbjct  51992  GGGAACTAGGC 52002

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Score = 204 bits (110), Expect = 2e-48
Identities = 213/261 (81%), Gaps = 14/261 (5%)
Strand=Plus/Plus

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Query  2250    CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA
|||||
Sbjct  40645    CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA
40704
Query  2308    GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCATTCCAGGCA--TGCAAGACCAGG
|||||
Sbjct  40705    GCGATTCTCCTGCCTCAGCTCCC--AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG
40761
Query  2365    -CTCAGCTAATTTTTGTATTTTT-GGTAGAGACGGGGTTTACCATAATGGCCAGTCTGG
|||||
Sbjct  40762    AC-CAGCTAATTTTTGTATTTTTAGG-AGAGATGGAGTTTGGCATGTGGGTAGGCTGG
40819
Query  2423    TCCTC-CATCTCCTGACCTCAGGTAATCCGCCCCGCCTCGGCCTCCCAAATTGCTGGGATTA
|||||
Sbjct  40820    TCTTGCA-CTCTGACCTTAAGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTA
40878
Query  2482    CAGGTATGAGCCACTGGGCC 2502
|||||
Sbjct  40879    TAGGCATGAGCCACCGTGCCC 40899

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>gb|AC040958.20| Homo sapiens chromosome 17, clone RP11-630H24, complete sequence
Length=26211

Score = 4806 bits (2602), Expect = 0.0
Identities = 2650/2670 (99%), Gaps = 16/2670 (0%)
Strand=Plus/Minus

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Query  1      GAATTACGACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60

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Sbjct	12201	 GCAGTGCCTCCCAACCATTCCTTATCCAGGCTTTTGTACACGCTATGCTCCGGGCC	12142
Query	957	GTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	1016
Sbjct	12141	 GTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATGG	12082
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	12081	 GTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAAGTAATGGGAGGAG	12022
Query	1077	ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATACGCTGAG	1136
Sbjct	12021	 ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATACGCTGAG	11962
Query	1137	TGAGGTTCCCGAGAAAGTAACAATGGGAGCAGTCTCCAGCATAGACCTTGGTGGGCGGT	1196
Sbjct	11961	 TGAGGTTCCCGAGAAAGTAACAATGGGAGCAGTCTCCAGCATAGACCTTGGTGGGCGGT	11902
Query	1197	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTTCCTGCAGAAC	1256
Sbjct	11901	 CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTTCCTGCAGAAC	11842
Query	1257	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAACACGC	1316
Sbjct	11841	 CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAACACGC	11782
Query	1317	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCAAGT-GGGATGGGGTAGACCTGTGGTCA	1375
Sbjct	11781	 AGCAGAAATCTGTGAGTGGATGCCTTCTCCCAAGTGGGGATGGGGTAGACCTGTGGTCA	11722
Query	1376	GAGCCCCGGGCGAGCAGCCACTGCCGGTCTTCCCTGCAGAACCTAGAGCTGCTCCG	1435
Sbjct	11721	 GAGCCCCGGGCGAGCAGCCACTGCCGGTCTTCCCTGCAGAACCTAGAGCTGCTCCG	11662
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTT	1495
Sbjct	11661	 CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGACGCTCCTCAGGAGCGTCTT	11602
Query	1496	CGCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGCTATCGCCACCTGAAGGACCT	1555
Sbjct	11601	 CGCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGCTATCGCCACCTGAAGGACCT	11542
Query	1556	AGAGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCA--GGAT--CCAATCCTGG	1612
Sbjct	11541	 AGAGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCAAGGATCCCAATCCTGG	11482
Query	1613	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	1672
Sbjct	11481	 GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	11422
Query	1673	GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCTTCGTAATCCTCCAGGCT	1732
Sbjct	11421	 GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCTTCGTAATCCTCCAGGCT	11362
Query	1733	TTCTCTACAACCTGGAGGGGAGGGAGGAGAAATGGATGAATGAGAGAGGGAGGGAACAGTG	1792
Sbjct	11361	 TTCTCTACAACCTGGAGGGGAGGGAGGAGAAATGGATGAATGAGAGAGGGAGGGAACAGTG	11302
Query	1793	CCCAAGCGCTTGGCTCTCCTTCTTCCTTCACITTCGAGAGGCTGGAAGATGGCAGCC	1852

Sbjct	11301		11242
Query	1853	CCCGGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAAAATCGCACAAACG	1912
Sbjct	11241	CCCGGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAAAATCGCACAAACG	11182
Query	1913	ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG	1972
Sbjct	11181	ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG	11122
Query	1973	TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC	2032
Sbjct	11121	TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC	11062
Query	2033	TGCCCCGGGTGGCATCCCTGTGACCCCTCCCGAGTGCCCTCTCGGTCGTGGAAGGTGCTA	2092
Sbjct	11061	TGCCCCGGGTGGCATCCCTGTGACCCCTCCCGAGTGCCCTCTCGGTCGTGGAAGGTGCTA	11002
Query	2093	CTCCAGTGCCCAACGACCCCTTGCTCTAATAAAATTAAGTTGCATCATTTTGTGTTGACTAGG	2152
Sbjct	11001	CTCCAGTGCCCAACGACCCCTTGCTCTAATAAAATTAAGTTGCATCATTTTGTGTTGACTAGG	10942
Query	2153	TGTCCTTGATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGCCAGGTTGGG	2212
Sbjct	10941	TGTCCTTGATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGC-AGGTTGGG	10883
Query	2213	AAGACAACCTGTAGGGCCCTCAGGGTCTATTTCGGGAACAGGCTGGAGTGCAGTGGCA-G	2271
Sbjct	10882	AAGACAACCTGTAGGGCCCTCAGGGTCTATT-TGGGAACAGGCTGGAGTGCAGTGGCAGG	10824
Query	2272	-TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAGCGATTCTCCTGCCTCAGTCTCC	2330
Sbjct	10823	ATCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAGCGATTCTCCTGCCTCAGTCTCC	10764
Query	2331	CGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA	2390
Sbjct	10763	CGAATAGTTGGGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA	10704
Query	2391	GAGACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCG	2450
Sbjct	10703	GAGACGGGGTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCG	10644
Query	2451	CCCGCCTCGGCCTCCCAAATTTGCTGGGATTACAGGTAATGAGCCACTGGGCCCTTCCCTGT	2510
Sbjct	10643	CCCGCCTCGGCCTCCCAAATTTGCTGGGATTACAGGTAATGAGCCACTGGGCCCTTCCCTGT	10584
Query	2511	CCTGTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT	2570
Sbjct	10583	CCTGTGATTTTAAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT	10524
Query	2571	GGCCATGCCAGCCAGTTGGACATTTGAGTTGTTTGGCTTGGCACTGTCTCTCATGCATT	2630
Sbjct	10523	GGCCATGCCAGCCAGTTGGACATTTGAGTTGTTTGGCTTGGCACTGTCTCTCATGCATT	10464
Query	2631	GGGTCCACTCAGTAGATGCTTGTGGAATTC	2660
Sbjct	10463	GGGTCCACTCAGTAGATGCTTGTGGAATTC	10434

Score = 2957 bits (1601), Expect = 0.0
 Identities = 2071/2291 (90%), Gaps = 59/2291 (2%)
 Strand=Plus/Minus

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Query 1 GAATTCAGCAGCTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT 60
Sbjct 4911 GAATTCAGGACTCAATGGTGCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT 4853

Query 61 TTTCCTCAACACACACATTCTGTCTGGTGGGTGGAGGGGAACATCGCGGGAGGAGGAAAG 120
Sbjct 4852 TTTCCTCAACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGAGGAGGAAAG 4793

Query 121 GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
Sbjct 4792 GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA 4734

Query 181 TCCTTCTCCCGCTTCAGGTTGGCCACCATTGGCCTGTGCGCAGAGGGGACCCACGIGACCC 240
Sbjct 4733 GCCTTCCCGCATTCAGGTTGACCAACATGGCCTGCGGCCAGAGGGGACCCACCTGACCC 4674

Query 241 TTAAGAGAGGACAAAGTTGGGTGGTA-TCTCTGGCTGACATTCTGTGCACAACCCCTACA 299
Sbjct 4673 TTAAGAGAGGACAAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGCACAATCCTTACA 4615

Query 300 ACGCTGGTGATGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT 359
Sbjct 4614 ACACCTGGTGATGGTGAGAAGGGAAGACGACAAGCCAGGGGGCATGATCCCAGCATGTGT 4555

Query 360 GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACAT 419
Sbjct 4554 GGGAGGAGCTTCCAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGATATAATGT 4495

Query 420 GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC 478
Sbjct 4494 ACACAGAAACAGGTGGGGTCAAGCAGGGAGAGAGAACTGGCCAGGGTATAAAAAGGGCCC 4435

Query 479 ACAAGAGACGAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTCTGTGG 538
Sbjct 4434 ACAAGAGACCGGCTCTAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTCTGTGG 4375

Query 539 ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAAATCCCTTT-GGCACAAT 596
Sbjct 4374 ACAGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAAATCCCTTTGGGCACAAC 4315

Query 597 GTGTCCTGAGGGGAGAGGCGGCTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT 656
Sbjct 4314 GTGTCCTGAGGGGAGAGGCGGCTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT 4255

Query 657 GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG-TATTGGGCAATCTCTGAATG 715
Sbjct 4254 GGGGCTTATGAATGTGAG-TATCGCCATCTAAGGCCAGATATTGGGCAATCTCTGAATG 4196

Query 716 TTCCTGGTCCCTGGAGGAGGAGAGAGAGAGAGAGAGAAAAAAACCAGCTCCTGGA 775
Sbjct 4195 TTCCTGGTCTCTGGA-G-GG-A-TG-GAGAGAGAGA-AAAAAACAA--CAGCTCCTGGA 4144

Query 776 ACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTGT-CCITCGGTTTCTCCCC 834
Sbjct 4143 GCAGGGAGAGCGCTGGCCTCTTGCTCTCCGGCTCCCTCCATTGGCCTCCGGTTTCTCCCC 4084

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Query	835	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAGA	894
Sbjct	4083	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGA	4024
Query	895	GGGC-AGTGCCITCCCAACCATTCCTTTATCCAGGCTTTTGGACAACGCTATGCTCCGCG	953
Sbjct	4023	-GGCTGGTGCCTGCCAAACCGTTCGGTTATCCAGGCTTTTGGACAACGCTATGCTCCAAAG	3965
Query	954	CCCGTCGC-CTGTACCACTGG-CATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGT	1011
Sbjct	3964	CCCATCGCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGTCTTGGGG	3907
Query	1012	AATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATGG	1070
Sbjct	3906	AATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGAAGTAATGG	3847
Query	1071	GAGGAGACTAAGGAGCTCAGGGTGTGTTTCTGAAGTGAAAATGCAGGCAGATGAGCATAC	1130
Sbjct	3846	GAGGAGACTAAGGAGCTCAGGGTGTGTTTCTGAAGCGAAAATGCAGGCAGATGAGCATAG	3787
Query	1131	GCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT-----AG-A	1182
Sbjct	3786	GCTGAGCCAGGTTCCAGAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACCAGCA	3727
Query	1183	---C---CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAG	1237
Sbjct	3726	GTCTCTCTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCCAAGGACCAGAAG	3667
Query	1238	TATTCATTCTTGCA-GAACCCTCAGACCTCCCTCTGCTTCTCAGAGTCTATTCACACCC	1296
Sbjct	3666	TATTCATTCTTGCAATG-ACTCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCAGACACC	3608
Query	1297	TTCCAACAGGGTGAAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCC-AGG-TGG	1354
Sbjct	3607	CTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCCTAGGCGGG	3548
Query	1355	GATGGGTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGCTCCTTCCCT	1414
Sbjct	3547	GATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGCTCCTTCCCT	3488
Query	1415	GCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCAATGGCTGGAGCCCGT	1474
Sbjct	3487	GCAGAACTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCTGGCTGGAGCCCGT	3428
Query	1475	GCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCTCCGACAGCAACGT	1534
Sbjct	3427	GCGGTTCCTCAGGAGTATGTTCCGCCAACCACTGGTGTATGACACCTCGGACAGCGATGA	3368
Query	1535	CTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGC	1594
Sbjct	3367	CTATCACCTCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGC	3308
Query	1595	ACCA-GGAT--CCAATCCTGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACACT	1650
Sbjct	3307	GCCAGGGGTGCGCAATCCTGGAACCCCACTGGCTTAGAGGG-CTGGGGAGAGAAACACT	3249
Query	1651	GCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCCGTATTCTTCATTTC	1710
Sbjct	3248	GCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCCGTATTCTTCATTTC	3189

Score = 941 bits (509), Expect = 0.0
Identities = 622/675 (92%), Gaps = 14/675 (2%)
Strand=Plus/Minus

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

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Query 1823 TCACTTTGCAGAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCT 1882
Sbjct 25972 TCACTTTGCAGAGGCTGGAAGACGGCAGCCGGACTGGGCAGATCCTCAAGCAGACCT 25913

Query 1883 ACAGCAAGTTTGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGC 1942
Sbjct 25912 ACAGCAAGTTTGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGC 25853

Query 1943 TCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCC 2002
Sbjct 25852 TCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCC 25793

Query 2003 GCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGTGGCATCCCTGTGACCCCTCCC 2062
Sbjct 25792 GCTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCGAGTAGCATCC-TGTGACCCCTCCC 25734

Query 2063 CAGTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCAGCCTTGTCTTAATAA 2122
Sbjct 25733 CAGTGCCTCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCACCAGCCTTGTCTTAATAA 25675

Query 2123 AATTAAGTTGCATCAATTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGA-GG 2181
Sbjct 25674 AATTAAGTTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGAAGG 25615

Query 2182 CGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCT 2240
Sbjct 25614 TGG-TGGTATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAGGTCT 25559

Query 2241 ATTCCGGGAACACGAC 2255
Sbjct 25558 AAT-GGGAAGTACGAC 25545

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Score = 209 bits (113), Expect = 5e-50
 Identities = 213/260 (81%), Gaps = 12/260 (4%)
 Strand=Plus/Minus

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Query 2250 CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA 2307
Sbjct 14047 CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA 13988

Query 2308 GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TGCAAGACCAGG 2364
Sbjct 13987 GCGATTCTCCTGCCTCAGCTCCC-AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG 13931

Query 2365 CTCAGCTAATTTTGTATTTT-GGTAGAGACGGGGTTCCACCATATTGGCCAGTCTGGT 2423
Sbjct 13930 CCCAGCTAATTTTGTATTTTAGG-AGAGATGGAGTTTGGCATGTGGGTTAGCCTGGT 13872

Query 2424 CTC-CATCTCTGACCTCAGGTAATCCGCCGCCCTCGGCCCTCCCAAATGTGGGATTAC 2482
Sbjct 13871 CTTGCA-CTCTGACCTTAAGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTAT 13813

Query 2483 AGGTATGAGCCACTGGGCC 2502
Sbjct 13812 AGGCATGAGCCACCGTGCCC 13793

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>gb|EU421715.1| Homo sapiens growth hormone 2 precursor (GH2) gene, complete

Sbjct	777	 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAAACG	836
Query	942	CTATGCTCCGCGCCCGTCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAA	1001
Sbjct	837	CTATGCTCCGCGCCCGTCGCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAA	896
Query	1002	GCTCTTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGG	1061
Sbjct	897	GCTCTTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGG	956
Query	1062	AAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGA	1121
Sbjct	957	AAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGA	1016
Query	1122	TGAGCATACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAG	1181
Sbjct	1017	TGAGCATACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAG	1076
Query	1182	ACCTTGGTGGGCGGTCTTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAGTATT	1241
Sbjct	1077	ACCTTGGTGGGCGGTCTTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAGTATT	1136
Query	1242	CATTCTGCAGAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCA	1301
Sbjct	1137	CATTCTGCAGAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCA	1196
Query	1302	ACAGGGTGAAAACGCAGCAGAAAATCTGTGAGTGGATGCCTTCTCCCGAGT-GGGATGGG	1360
Sbjct	1197	ACAGGGTGAAAACGCAGCAGAAAATCTGTGAGTGGATGCCTTCTCCCGAGTGGGATGGG	1256
Query	1361	GTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTCGAGAA	1420
Sbjct	1257	GTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTCGAGAA	1316
Query	1421	CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCT	1480
Sbjct	1317	CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCT	1376
Query	1481	CCTCAGGAGCGCTTTCGCCAACAGCCTGGTGATGGCGCTCGGACAGCAACGTCTATCG	1540
Sbjct	1377	CCTCAGGAGCGCTTTCGCCAACAGCCTGGTGATGGCGCTCGGACAGCAACGTCTATCG	1436
Query	1541	CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAG-G	1599
Sbjct	1437	CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG	1496
Query	1600	GAT--CCAATCTGGGGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCC	1657
Sbjct	1497	GATCCCCAATCTGGGGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCC	1556
Query	1658	TCITTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACGCTATCTTTCATTTCCCTCTGT	1717
Sbjct	1557	TCITTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACGCTATCTTTCATTTCCCTCTGT	1616
Query	1718	GAATCCTCCAGGCCCTTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAG	1777
Sbjct	1617	GAATCCTCCAGGCCCTTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAG	1676
Query	1778	AGGGAGGGAACAGTGCCCAAGCGCTTGCCCTCTCCTTCTCTCTCTTCTTGTGACAGGC	1837

Sbjct	1677	AGGGAGGGGAACAGTGCCTCAAGCGCTTGCCCTCTCCTTCTCTCTCTCCTTTCACCTTTCAGAGGGC	1736
Query	1838	TGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACA	1897
Sbjct	1737	TGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACA	1796
Query	1898	CAAAATCGCACACGATGACGCACCTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGA	1957
Sbjct	1797	CAAAATCGCACACGATGACGCACCTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGA	1856
Query	1958	AGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGGCGCTCTGTGGAGGGCA	2017
Sbjct	1857	AGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGGCGCTCTGTGGAGGGCA	1916
Query	2018	GCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGG	2077
Sbjct	1917	GCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGG	1976
Query	2078	TCGTGGAAGGTGCTACTCCAGTGCCACCAGCCCTGTGCTTAATAAAATTAAGTTGCATCA	2137
Sbjct	1977	TCGTGGAAGGTGCTACTCCAGTGCCACCAGCCCTGTGCTTAATAAAATTAAGTTGCATCA	2036
Query	2138	TTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCA	2197
Sbjct	2037	TTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCA	2096
Query	2198	AGGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCCTTCAGGGTCTATTTCGGGAACCAGGCTG	2257
Sbjct	2097	AGGGGC-AGGTTGGGAAGACAACCTGTAGGGCCCTTCAGGGTCTATT-TGGGAACCAGGCTG	2154
Query	2258	GAGTGCAGTGGCA-G-ICTTGGCTCGCTGCAATCTCCGCC	2295
Sbjct	2155	GAGTGCAGTGGCACGATCTTGGCTCGCTGCAATCTCCGCC	2194

>gb|AC127029.12| Homo sapiens chromosome 17, clone CTC-264K15, complete sequence
Length=101990

Score = 3864 bits (2092), Expect = 0.0
Identities = 2487/2675 (92%), Gaps = 37/2675 (1%)
Strand=Plus/Minus

Query	1	GAATTCAGCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTTTGGCCCCCT	60
Sbjct	28460	GAATTCAGGACTGAATCTGTGCTCACACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT	28402
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	28401	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG	28342
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTA-GGGGTCTCAAGGACTGGCCTATCCTGAC	179
Sbjct	28341	GGATAGGATAGAGAATGGGATGTGGTCGGTAGGGGGTCTCAAGGACTGG-CTATCCTGAC	28283
Query	180	ATCCTTCTCCGCGTTTACAGTTTGGCCACCATTGGCCTGCTGCCAGAGGGCACCACGTGACC	239
Sbjct	28282	ATCCTTCGCGCGTGCAGGTGGCCACCATTGGCCTGCGGCGCAGAGGGCACCACGTGACC	28223
Query	240	CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCGTGCACAACCCCTACA	299

Sbjct	28222		CTTAAAGAGAGGACAGATTGGGTGGTATCTCTGGCTGACACTCTGTGCACAAACCTCACA	28163
Query	300	ACGCTGGTGTATGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGT	359	
Sbjct	28162		ACACTGGTGACGGTGGGAAGGGAAGATGACAAGCCAGGGGGCATGATCCAGCATGTGT	28103
Query	360	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCATAACAT	419	
Sbjct	28102		GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	28043
Query	420	GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAGGGCCC	478	
Sbjct	28042		ACACAGAAACAGGTGGGGTCAA-CAGTGGGAGAGAAGGGGCCAGGGTATAAAAGGGCCC	27984
Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGG	538	
Sbjct	27983		ACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGG	27924
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCTTAAATCCCTTT-GGCACAAT	596	
Sbjct	27923		ACAGCTCACCTAGCTGCAATGGCTACAGGTAAGCGCCCTTAAATCCCTTTGGGCACAAT	27864
Query	597	GTGTCTCTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT	656	
Sbjct	27863		GTGTCTCTGAGGGGAGAGGCGACCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT	27804
Query	657	GGGGCTTATGAATGTTAGCTATCGCATCTAAGCCAGTATTGGCCAATCTCTGAATGT	716	
Sbjct	27803		GGGGCTTCTGAATGTGAG-TATCGCATGTAAGCCAGTATTGGCCAATCTCAGAAAGC	27745
Query	717	TCCTGGTCCCTGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	776	
Sbjct	27744		TCCTGGTCCCT---GGA-G--G-GA-TG-GAGAGAG-AAAAACAA--CAGCTCCTGGAG	27697
Query	777	CAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCA	835	
Sbjct	27696		CAGGGAGAGTGCTGGCCTCTTGCTCTCCGGCTCCCTCTGTTGCCCTCTGGTTTCTCCCA	27637
Query	836	GGCTCCCGGACGTCCTGTCTCTGGCTTTTGCCCTGCTCTGCTGCTGCTGCTGCTTCAAGAG	895	
Sbjct	27636		GGCTCCCGGACGTCCTGTCTCTGGCTTTTGCCCTGCTCTGCTGCTGCTGCTGCTTCAAGAG	27577
Query	896	GGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTGACACGCTATGCTCCCGGCC	955	
Sbjct	27576		GGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTGACACGCTATGCTCCCGGCC	27517
Query	956	CGTCGCTGTACACAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGGTAATG	1015	
Sbjct	27516		CATCGTCTGACACAGCTGGCCTTTGACACCTACCAGGAGTTTGTAAAGCTCTTGGGTAATG	27457
Query	1016	GGTGGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATG-GGAGG	1074	
Sbjct	27456		GGTGGCATACAGGGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAAGTAA-GAGGAGG	27398
Query	1075	AGACTAAGGAGCTCAGGGTGTGTTTCTGAAGTGAAATGACAGGCAGATGAGCATACGCTG	1134	
Sbjct	27397		AGACTAAGGAGCTCAGGGT-TTCCCGAAGCGAAATGACAGGCAGATGAGCACACGCTG	27339
Query	1135	AGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGTGGGCG	1194	

Sbjct	27338		AGTGAGGTTCCCGAGAAAGTAACAATGGGAGCTGGTCTTCAGAGCTAGACCTTGGTGGGGC	27279
Query	1195	GTCTTCTCTCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCCTGCAGAA	1254	
Sbjct	27278	GTCTTCTCTCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGTATTCATTCCTGCAGAA	27219	
Query	1255	CCCCCAGACCTCCCTCTGTCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAC	1314	
Sbjct	27218	CCCCCAGACCTCCCTCTGTCTTCTCAGAGTCTATTCCGACACCTTCCAACAGGGAGGAAC	27159	
Query	1315	GCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGG-TGGGATGGGGTAGACCTGTGGT	1373	
Sbjct	27158	ACAACAGAAATCCGTGAGTGGATGCCTTCTCCCCAGGCGGGATGGGGAGACCTGTAGT	27099	
Query	1374	CAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTGCAGAACCTAGAGCTGCTC	1433	
Sbjct	27098	CAGAGCCCCCGGGCAGCACAGCCAATGCCGTCCTTCCCTGCAGAACCTAGAGCTGCTC	27039	
Query	1434	CGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTC	1493	
Sbjct	27038	CGCATCTCCCTGCTGCTCATCCAGTCGCTGGCTGGAGCCCGTGCAGTCTCCTCAGGAGTGC	26979	
Query	1494	TTCCGCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATCG-CCACCTGAAGGA	1552	
Sbjct	26978	TTCCGCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGCTCTAT-GACCTCTAAAGGA	26920	
Query	1553	CCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGCCACCA-GGAT--CCAATCC	1609	
Sbjct	26919	CCTAGAGGAAGGCATCCAAACGCTGATGGGGTGAGGGTGCGGCCAGGGGTCCCCCAATCC	26860	
Query	1610	TGGGGCCCCACTTGGCTTCCAGGGACTG-GGGAGAGAAACACTGCTGCCCTCTTTTAGCA	1668	
Sbjct	26859	TGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGCTGCCCTCTTTTAGCA	26801	
Query	1669	GTCAGGCGCTGACCCAAGAGAAGTACCCTGTTCTTCTATTTCCCTCTGTGAATCCTCCAG	1728	
Sbjct	26800	GTCAGGCGCTGACCCAAGAGAAGTACCCTTATTCTTCTATTTCCCTCTGTGAATCCTCCAG	26741	
Query	1729	GCCTTCTCTACAACTGGAGGGGAGGGAGGAAAAATGGATGAATGAGAGGGGAGGGAAAC	1788	
Sbjct	26740	GCCTTCTCTACAACTGAAGGGGAGGGAGGAAAAATGAATGAATGAGAAAGGGAGGGAAAC	26681	
Query	1789	AGTGCCCAAGCGCTTGGCCTCTCCTTCTCTCTTCACTTTGAGAGGCTTGAAGATGGC	1848	
Sbjct	26680	AGTACCCAAGCGCTTGGCCTCTCCTTCTCTCTTCACTTTGAGAGGCTTGAAGATGGC	26621	
Query	1849	AGCCCCGGGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAAAATCGCAC	1908	
Sbjct	26620	AGCCCCGGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTTGACACAAAATCGCAC	26561	
Query	1909	AACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	1968	
Sbjct	26560	AACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	26501	
Query	1969	AAGGTCGAGACATTCCTGCGCATCGTGAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTC	2028	
Sbjct	26500	AAGGTCGAGACATTCCTGCGCATCGTGAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTC	26441	
Query	2029	TAGTGTCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCTCTCTGTGCTGGAAGGT	2088	


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Sbjct  26440  ||||||||||||||||||||||||||||||||||||||||||||| 26381
TAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTCTGGCCCTGGGAAGTT

Query  2089  GCTACTCCAGTGCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTGAC 2148
|| |||||||||||||||||||||||||||||||||||||||||

Sbjct  26380  GCCACTCCAGTGCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTGAC 26321

Query  2149  TAGGTGTCTCTGTATAATATTATGCGGTGGAGCGGGTGGTATGGAGCAAGGGGCCAGGT 2208
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  26320  TAGGTGTCTCTATAATATTATGCGGTGGAGGGGGTGGTATGGAGCAAGGGGCAAG-T 26262

Query  2209  TGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTCGGGAACCAAGCGTGGAGTGCAGTGG 2268
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  26261  TGGGAAGACAACCTGTAGGGCCTGCGGGGTCTATT-GGGAACCAAGCTGGAGTGCAGTGG 26203

Query  2269  CAG--TCITGGCTCGTGCAATCTCCGCCCTCTGGGTTCAGCGATTCTCTGCCTCAGT 2326
|| |||||||||||||||||||||||||||||||||||||||||

Sbjct  26202  CACAATCTTGGCTCACTGCAATCTCCGCCCTCTGGGTTCAGCGATTCTCTGCCTCAGC 26143

Query  2327  CTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTT 2386
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  26142  CTCCCGAGTTGTTGGGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTT 26083

Query  2387  GGTAGAGACGGGGTTTACCACATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGTAA 2446
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  26082  GGTAGAGACGGGGTTTACCACATATTGGCCAGGCTGGTCTCCAACCTCTAATCTCAGTGA 26023

Query  2447  TCCGCCCGCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCC 2506
|| ||| ||| ||||||||||||||||||||||||| ||| ||||| |||||||

Sbjct  26022  TCTACCCACCTTGGCTCCTCCCAAATTGCTGGGATTACAGGCGTGAACCACTGCTCCCTTCC 25963

Query  2507  CTGTCTCTG-TGATTTTAAATAAATTATACCAGCAGAAGGAGCTCCAGACACAGCATGGGC 2565
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  25962  CTGTCTCTCTGATTTTAAATAAATACTATACCAGCAGGAGGAGCTCCAGACACAGCATAGGC 25903

Query  2566  TACCTGGCCATGCCAGCCAGTTGGACATTTGAGTTGTTTGGCTTGGCACTGTCTCTCAT 2625
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  25902  TACCTGGCCATGCCAACCGGTGGGACATTTGAGTTGCTTGGCTTGGCACTGTCTCTCAT 25843

Query  2626  GCATTGGGTCCACTCAGTAGATGCTTGTGGAATTC 2660
|| ||||||||||||||||||||| |||||||||

Sbjct  25842  GCGTTGGGTCCACTCAGTAGATGCTTGTGGAATTC 25808

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Score = 2987 bits (1617), Expect = 0.0
 Identities = 2074/2288 (90%), Gaps = 57/2288 (2%)
 Strand=Plus/Minus

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Query  1  GAATTCAGCAGTGAATCATGCCAGAACCCCCGAATCTATTGGCTGTGCTTTGGCCCCCT 60
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  6195  GAATTCAGGACTCAATGGTGCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT 6137

Query  61  TTTCACACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
|||||||||||||||||||||||||||||||||||||||||||

Sbjct  6136  TTTCACACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGGAGGAGGAAAG 6077

Query  121  GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCTGACA 180
||||||||||||||||||| ||||||||||||||||||||| |||||||||||

Sbjct  6076  GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCTGACA 6018

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Query	181	TCCTTCTCCGCTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACGCTGACCC	240
Sbjct	6017	GCCTTCCCCGCGTTTCAGGTTGACCAACATGGCCTGCAGCCAGAGGGGCACCCACCTGACCC	5958
Query	241	TTAAAGAGAGGACAAAGTTGGGTGGTA-TCTCTGGCTGACATTCTGTGCACAACCCCTCACA	299
Sbjct	5957	TTAAAGAGAGGACAAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGCACAATCCTTACA	5899
Query	300	ACGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT	359
Sbjct	5898	ACACTGGTGATGGTGAGAAGGAAAGACGACAAGCCAGGGGGCATGATCCCAGCATGTGT	5839
Query	360	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCCTAAACAT	419
Sbjct	5838	GGGAGGAGCTTCTAAATTATCCACTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	5779
Query	420	GCAGAGAAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC	478
Sbjct	5778	ACACAGAAAACAGGTGGGGTCAAGCAGGGAGAGAGAAGTGGCCAGGGTATAAAAAGGGCCC	5719
Query	479	ACAAGAGAGACAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTCTGTGG	538
Sbjct	5718	ACAAGAGACCGGCTCTAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTCTGTGG	5659
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAAGCGCCCCATAAATCCCTTT-GGCACAAT	596
Sbjct	5658	ACAGCTCACCTAGTGGCAATGGCTCCAGGTAAGCGCCCCATAAATCCCTTTGGGCACAAC	5599
Query	597	GTGTCCTGAGGGGAGAGGCGCGCTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	656
Sbjct	5598	GTGTCCTGAGGGGAGAGGCGCGCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	5539
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG-TAATTGGCCAATCTCTGAATG	715
Sbjct	5538	GGGGCTTATGAATGTGAG-TATCGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATG	5480
Query	716	TTCTTGGTCCCTGGAGGAGGAGAGAGAGAGAGAGAAAAAA-AAACCCAGCTCCTGG	774
Sbjct	5479	TTCTTGGTCTCTGGA-G-GG-A-TG-GAGAGAGAGA-AAAAAACAAA--CAGCTCCTGG	5428
Query	775	AACAGGGAGAGCGCTGGCCCTTTGCTCTCCAGCTCCCTCTGTG-CCTCCGGTTTCTCCC	833
Sbjct	5427	AGCAGGGAGAGCGCTGGCCCTTTCTCTCCGGCTCCCTCCATTGCCCTCCGGTTTCTCCC	5368
Query	834	CAGGCTCCCGGACGCTCCTGCTCCTGGCTTTTGGCCTGCTCTGCTGCTGGCTTCAAG	893
Sbjct	5367	CAGGCTCCCGGACGCTCCTGCTCCTGGCTTTTGGCCTGCTCTGCTGCTGGCTTCAAG	5308
Query	894	AGGGC-AGTGCCTTCCCAACCAATCCCTTATCCAGGCTTTTGTACAACGCTATGCTCCGC	952
Sbjct	5307	A-GGCTGGTGCGCTCCAAACCGTTCCCTTATCCAGGCTTTTGTACCACGCTATGCTCCAA	5249
Query	953	GCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAAGCTCTTGGG	1010
Sbjct	5248	GCCCATCTCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGTCTTGGG	5191
Query	1011	TAATGGGTGCGCTTACAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATG	1069
Sbjct	5190	GAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGAAGTAATG	5131

Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATA	1129
Sbjct	5130	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAAATGCAGGCAGATGAGCATA	5071
Query	1130	CGCTGAGTGAGGTTCCCGAGAAAAGTAAACATGGGAGCAGGTTCCAGCAT-----AG-	1181
Sbjct	5070	GGCTGAGCCAGGTTCCCGAGAAAAGCAACATGGGAGCTGGTCTCCAGCATAGAAACGAGC	5011
Query	1182	A---C---CTTGGTGGGCGGTCTTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAA	1236
Sbjct	5010	AGTCCTTCTTGGTGGGCGGTCTTCTCTAGGAAGAACTATATCCAAAGGACCAGAA	4951
Query	1237	GTATTCACTTCTGCA-GAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAAACAC	1295
Sbjct	4950	GTATTCACTTCTGCAAT-ACTCCAGACCTCCTTCTGCTTCTCAGAGTCTATTCCGACAC	4892
Query	1296	CTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCTTCTTCCCC-AGG-TG	1353
Sbjct	4891	CCTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCTAGGCGG	4832
Query	1354	GGATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCC	1413
Sbjct	4831	GGATGGGGTAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGGTCTTCCCC	4772
Query	1414	TGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCTATGGCTGGAGCCCG	1473
Sbjct	4771	TGCAGAACTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCTGCTGGCTGGAGCCCG	4712
Query	1474	TGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACG	1533
Sbjct	4711	TGCGGTTCTCTAGGAGTATGTTCCGCCAACACCTGGTGTATGACACCTCGGACAGCGATG	4652
Query	1534	TCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGG	1593
Sbjct	4651	ACTATACCTCTCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGG	4592
Query	1594	CACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACAC	1649
Sbjct	4591	CGCCAGGGGTACCAATCCTGGAACCCCACTGGCTTCGAGGG-CTGGGGGAGAGAAATAC	4533
Query	1650	TGCTGCCCTCTTTTATGAGTACAGGCGTGACCCAAGAGAACTACACGTATCTTTCATTT	1709
Sbjct	4532	TGCTGCCCTCTTTTATGAGTAAAGCGCTGACCCAAGAGAACTACCTTATTCTTTCATTT	4473
Query	1710	CCCCTCGTGAATCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAAATGGATG	1769
Sbjct	4472	CGCCTGGTGAATCTCCAGGCCTTTCTCTACACCTGAAGGGGAGGGAGGAAAAATGGATA	4413
Query	1770	AATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCCTTCTCTTCTTCACTTT	1829
Sbjct	4412	AATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCCTTCTCTTCTTCACTTT	4353
Query	1830	GCAGAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCTACAGCAA	1889
Sbjct	4352	GCAGAGGCTGGAAGACGGCAGCCGCGGACTGGGCAGATCTCAAGCAGACCTACAGCAA	4293
Query	1890	GTTTGACACAAAAATCGCACAAACGATGACGCACTGCTCAAGAAGTACGGGCTGCTCTACTG	1949
Sbjct	4292	GTTTGACACAAATCGCACAAACGATGACGCACTGCTCAAGAAGTACGGGCTGCTCTACTG	4233

Query	1950	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGCCGCTCTGT	2009
Sbjct	4232	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGCCGCTCTGT	4173
Query	2010	GGAGGGGACAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCC	2069
Sbjct	4172	GGAGGGGACAGCTGTGGCTTCTAGGTGCCCGAGTAGCATCC-TGTGACCCCTCCCCAGTGCC	4114
Query	2070	TCTCCTGGTCTGTGGAAGGTGCTACTCCAGTGCCACCAGCCCTTGTCTAATAAAATTAAG	2129
Sbjct	4113	TCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCACCAGCCCTTGTCTAATAAAATTAAG	4055
Query	2130	TTGCATCATTTTGGTTTGACTAGGTGTCCTTGTATAATATTATGGGGTGA-GGCGGGTGG	2188
Sbjct	4054	TTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGAAGGTGG-TGG	3996
Query	2189	TATGGAGCAAGGGGCCAGGTGTGGGAAGACA-ACCTGTAGGGCCCTCAGGGTCTATTGGG	2247
Sbjct	3995	TATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCCTCAAGGTCTATT-GGG	3940
Query	2248	AACCAGGC 2255	
Sbjct	3939	AACTAGGC 3932	

Score = 2966 bits (1606), Expect = 0.0
 Identities = 2074/2291 (90%), Gaps = 68/2291 (2%)
 Strand=Plus/Minus

Query	1	GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCTT	60
Sbjct	20879	GAATTCAGGACTGAATCATGCTCACAACCCCAACAATCTATTGGCTGTGC-TTGGCCCTT	20821
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	20820	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG	20761
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCATCTCTGACA	180
Sbjct	20760	GAATAGGATAGAGAGTGGGATGTGGTCGATAGGGGTCTCAAGGACTGG-CTATCTGACA	20702
Query	181	TCCTTCTCCGCGTTACAGGTGGCCACCATTGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	20701	TCCTTCTCCGCAATTCAGGTGGCCACCATTGGCCTGCTGCCAGAGGGCACCCACCTGAACC	20642
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCGTGACACAACCCCTCACAA	300
Sbjct	20641	TTAAAGAGAGGACAAGTTGGGTGGTGTCTGTGGTTGACACTCTGTGACACAACCCCTCACAA	20582
Query	301	CGCTGGTGATGGTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG	360
Sbjct	20581	CGCTGGTGACGGTGGGAAGGGAAGATGACAAGCCAGGGGACATGATGCCAGCATGTGTG	20522
Query	361	GGAGGAGCTTCTAAATATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGGCTTAACATG	420
Sbjct	20521	GGAGGAGCTTCCAAATATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGTG	20462
Query	421	CAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAGGGCCC	478
Sbjct	20461	CACAGAAACAGGTG-GGGGCAA-CAGCGAGAGAGAAGGGGCCAGGGTATAAAAGGGCCC	20404

Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGG	538
Sbjct	20403	ACAAGAGACCAGCTCCAGCATCCCAAGGCCGACCTCCCCGACCACTCAGGGTCTGTGG	20344
Query	539	ACAGCTCA-CTAGCGCAATGGCTGCAGGTAAGCGCCCTAAAAATCCCTTT-GGCACAAT	596
Sbjct	20343	ACAGCTCACCTAGCGCAATGGCTGCAGGTAAGCGCCCTAAAAATCCCTTTGGGCACAAC	20284
Query	597	GTGTCTCTGAGGGGAGAGGCGGCGCTCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT	656
Sbjct	20283	GTGTCTCTGAGGGGAGAGGCGGCGCTCTGCAGATGGGACGGGGGCACTAA-CCTCAGGTTT	20225
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG-TATTTGGCCAATCTCTGAATG	715
Sbjct	20224	GGGGCTTCTGAATGTGA-ATATCGCCATCTAAGGCCAGATATTGGCCAATCTCTGAATG	20166
Query	716	TTCTTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAAAAAAACCCAGCTCCTGGA	775
Sbjct	20165	TTCTTGGTCCCT---GGAGG--GA-TG-GAGAGAGAGAGAAAAAGAAAA--CAGCTCCTGGA	20115
Query	776	ACAGGGAGAGCGCTGGCCCTCTGTCTCTCCAGCTCCCTCTGTG-CCTCCGGTTTCTCCCC	834
Sbjct	20114	ACAGGGAGAGTGCTGGCCCTCTGTCTCTCGGGCTCCCT-TCTTGCCCTCCGGTTTCTCCCC	20056
Query	835	AGGCTCCCGACGCTCCCTGCTCCTGGCTTTTGCCCTGCTCTGCTTGGCTTCAAGA	894
Sbjct	20055	AGGCTCCCGACGCTCCCTGCTCCTGGCTTTTGCCCTGCTCTGCTGCCCTGGCTTCAAGA	19996
Query	895	GGGC-AGTGCCTTCCCAACCATCCCTTAITCCAGGCTTTTTGACA-ACGCTATGCTCCGC	952
Sbjct	19995	-GGCTGGTGCCGCTCCAAACCGTTCCCTTATCCAGGCTTTTT-AAAGAGGCTATGCTCCAA	19938
Query	953	GCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAGCTCTTGGG	1010
Sbjct	19937	GCCCATCGGC-ACACAGCTGGCCAT-TGACACGTACAGGAGTTTATAAGCTCTTGGG	19880
Query	1011	TAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAAITTTCCCGCT-GGGAAGTAATG	1069
Sbjct	19879	GAATGGGTGCGGTTCAGGGTGGCAAGAAGGGGTGACTTTCCCCACTGGGGAAGTAATG	19820
Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATA	1129
Sbjct	19819	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAATGCAGGCAGATGAGCATA	19760
Query	1130	CGTGTAGTGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGCTCCAGCAT---AG-A--	1182
Sbjct	19759	GGCTGAGCCAGGTTCCCAGAAAGTAACAGTGGGAGCTGGTCTCCAGCATAGAAAGCAGT	19700
Query	1183	---C---CTTGGTGGGCGGCTCTTCTCTAGGAAGAAGCCATATATC-CTGAAGGAGCAGA	1235
Sbjct	19699	GGTCTTCTTGGTGGGGGTCCTTCCCCTAGGAAGAAGCCATATATCAC-AAAGGAACAGA	19641
Query	1236	AGTATTCATTCTGCA-GAACCCCGAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACA	1294
Sbjct	19640	AGTATTCATTCTGCAATG-ACCTCCAGACCTCCTTCTGCTTCTCAGAGTCTATTCCGACA	19582
Query	1295	-CCTTCCAACAGGGTGAAACGAGCAGAGAAATCTGTGAGTGGATGCCT-TCTCCCC-AGG	1351
Sbjct	19581	TCC-TCCAACATGGAGGAACGAGCAGAGAAATCCGTGAGTGGATG-CTGTCTCCCTTAGG	19524

Query	1352	-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGAGCAGCAGCCACTGCGCGTCTTC	1410
Sbjct	19523	CGGGGATGGGGGAGACCTGTGGTCAGAGCCCCGGGAGCAGCAGCCACTGCGCGTCTTC	19464
Query	1411	CCCTGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGC	1470
Sbjct	19463	CCCTGCAGAACCTAGAGCTGCTCCACATCTCCCTGCTGCTCATCGAGTCGCGGCTGGAGC	19404
Query	1471	CCGTGCGAGCTCTCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCA	1530
Sbjct	19403	CCGTGCGGTTCTCTCAGGAGTACCTTCACCAACAACCTGGTGTATGACACCTCGGACAGCG	19344
Query	1531	ACGTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGG	1590
Sbjct	19343	ATGACTATCACTCTCTAAAGGACCTAGAGGAAGGCATCCAAATGCTGATGGGGTGAGGG	19284
Query	1591	TGGCACCA--GGAT--CCAATCCTGG--GGCCCCACTGGCTTCCAGGGACT--GGGGAGAGAA	1645
Sbjct	19283	TGGCACCAAGGGTCCCCAATCTCGGAAG--CCCACTGGCTTCGAGGG--CTGGGGAGAGAA	19226
Query	1646	ACACTGCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAAGTACCGTATTCTTC	1705
Sbjct	19225	ACACTGCTGCCCTCTTTTACGAGTCAGGCGCTGACCCAAGAGAAGTACCGTATTCTTC	19166
Query	1706	ATTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATG	1765
Sbjct	19165	ATTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACACCTGAAGGGGAGGAGGAAAATG	19106
Query	1766	GATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCCTCTCCTTCTCTCTCTCA	1825
Sbjct	19105	GATAAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGTGCTCTCCTTCTCTGTGCTCA	19046
Query	1826	CTTTGCAGAGGCTGGAAGATGGCAGCCCCGGAGTGGGCAGATCTTCAATCAGTCTACA	1885
Sbjct	19045	CTTTGCAGAGGCTGGAAGACGCGAGCCACTGACTGGGCAGACCTCAAGGAGACCTACA	18986
Query	1886	GCAAGTTTGACACAAAATCGCACACAGATGACGCAGTCTCTCAAGAACTACGGGCTGCTCT	1945
Sbjct	18985	GCAAGTTTGACACAAACTCGCACAACTGACGCAGTCTCTCAAGAACTACGGGCTGCTCT	18926
Query	1946	ACTGCTTCAGGAAGGACATGGACAAGGTGCGAGACATTCCTGCGCATCTGTGCAGTGCCGCT	2005
Sbjct	18925	ACTGCTTCAGGAAGGACATGGACAAGGTGCGAGACATTCCTGCGCATGTGTGCAGTGCCGCT	18866
Query	2006	CTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCGGGTGGCATCCTGTGACCCCTCCCCAG	2065
Sbjct	18865	CTGTGGAGGGCAGCTGTGGCTTCTAGGGGCCGCGTGGCATCC--TGTGACCCCTCCCCAG	18807
Query	2066	TGCCTCTCTGGTCTGGAAGGTGCTACTCCAGTGCCCAACGAGCCTGTGCTTAATAAAAT	2125
Sbjct	18806	TGCCCTCTCTGGCCCTG--AAGGTGCCACTCCAGTGCCCAACGAGCCTGTGCTTAATAAAAT	18748
Query	2126	TAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA--GGCGG	2184
Sbjct	18747	TAAGTTGTATTGTTTCATCTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAAGGTGG	18688
Query	2185	GTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCTCTCAGGGTCTATTCT	2244
Sbjct	18687	-TGGTATGGAGCAAGGGGT--AGGT--GGGAAGACGACCTGGAGGGCTCTCAGGGTCTATT-	18632

Sbjct	1596		1655
		CCAATCTCGAGCCCCACTGACTTTGAGAGACTGTGTTAGAGAAACACTGGCTGCCCTCT	
Query	1661	TTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCTCTGTA	1720
Sbjct	1656	TTTTAGCAGTCAGGCCCCGACCCAAGAGAACTACCTTATTCTTCATTTCCTCTGTA	1715
Query	1721	TCTCCAGGCGCTTCTCTACAACCTGGAGGGGAGGAGGAAATGGATGAATGAGAGAGG	1780
Sbjct	1716	TCTCCAGGCGCTTCTCTAC-A-CTGAAGGGGAGGAGGAAATGAATGAATGAGAAAGG	1773
Query	1781	GAGGGAACAGTGCCCAAGCGCTTGGCCCTCCTTCTCTCTCTTTCACCTTTGACAGAGGCTGG	1840
Sbjct	1774	GAGGGAACAGTACCCAAGCGCTTGGCCCTCCTTCTCTCTCTTTCACCTTTGACAGAGGCTGG	1833
Query	1841	AAGATGGCAGCCCCCGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAA	1900
Sbjct	1834	AAGATGGCAGCCCCCGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTTCGACACAA	1893
Query	1901	AATCGCACACAGTATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGG	1960
Sbjct	1894	ACTCACACACAGTATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGG	1953
Query	1961	ACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGGCGCTCTGTGGAGGGGAGCT	2020
Sbjct	1954	ACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGGCGCTCTGTGGAGGGGAGCT	2013
Query	2021	GTGGCTTCTAGTGCCTGGGTTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGTTCG	2080
Sbjct	2014	GTGGCTTCTAGTGCCTGGGTTGGCATCCCTGTGACCCCTCCCAAGTGCCTCTCTGGGCC	2073
Query	2081	TGGAAGGTGCTACTCCAGTGCCCAACGAGCCTTGCTCTAATAAAATTAAAGTTGCATCATTT	2140
Sbjct	2074	TGGAAGTTGCCACTCCAGTGCCCAACGAGCCTTGCTCTAATAAAATTAAAGTTGCATCATTT	2133
Query	2141	TGTTTGACTAGGTGTCCTTGATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGG	2200
Sbjct	2134	TGTCGACTAGGTGTCCTTCTATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGG	2193
Query	2201	GGCC-AGGTTGGGAAGACAACCTGTAGGGCTTCAGGGTCTATTCCGGGAACCAAGGCTGGA	2259
Sbjct	2194	GGCCCAAGTTGGGAAGACAACCTGTAGGGCTCGGGGGTCTATTCCGGGAACCAAGGCTGGA	2253
Query	2260	GTGCAGTGGCAG--TCTGGCTCGTGCAATCTCCGCCCTCTGGGTTCAAGCGATTCTCC	2317
Sbjct	2254	GTGCAGTGGCACAATCTTGGCTCACTGCAATCTCCGCCCTCTGGGTTCAAGCGATTCTCC	2313
Query	2318	TGCCTCAGTCTCCCGAATAGTTGCGATTCCAGGCATGCAAGACAGGCTCAGCTAATTTT	2377
Sbjct	2314	TGCCTCAGCTCCCGAGTTGTTGGGATTCCAGGCATGCAAGACAGGCTCAGCTAATTTT	2373
Query	2378	TGATATTTTGGTAGAGACGGGGTTTACCATAATTGGCCAGTCTGGTCTCCAATCTCTGAC	2437
Sbjct	2374	TGTTTTTTTGGTAGAGACGGGGTTTACCATAATTGGCCAGGCTGGTCTCCAATCTCTAAT	2433
Query	2438	CTCAGGTAATCCGCCCGCTCGGCCCTCCCAAATTTGCTGGGATTACAGGTATGAGCCACTG	2497
Sbjct	2434	CTCAGGTGATCTACCCACCTTGGCCCTCCCAAATTTGCTGGGATTACAGGCGTGAACCACTG	2493
Query	2498	GGCCCTTCCCTGTCTGT-TGATTTTAAATAATTATACCAGCAGAAGGACGTCCAGACAC	2556

Query	1022	CTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGG--AAGTAATGGGAGGAGACTA	1080
Sbjct	134255	CTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGGAAGTAATGGGAGGAGACTA	134314
Query	1081	AGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATACGCTGAGT	1140
Sbjct	134315	AGGAGCTCAGGGTTGTTTTCTGAAGTGAATAATGCAGGCAGATGAGCATACGCTGAGT	134374
Query	1141	GTTCACAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTCTT	1200
Sbjct	134375	GTTCACAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGTCTT	134434
Query	1201	CTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCATTCCTGCAGAACCCCCA	1260
Sbjct	134435	CTCCTAGGAAGAAGCCTATATCTCTGAAGGAGCAGAAGTATTCATTCCTGCAGAACCCCCA	134494
Query	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCACACACCTTCCACAGGGTGAAAACGCAGCA	1320
Sbjct	134495	GACCTCCCTCTGCTTCTCAGAGTCTATTCACACACCTTCCACAGGGTGAAAACGCAGCA	134554
Query	1321	GAAATCTGTGAGTGGATGCCITCTCCCAAGGTGGG--ATGGGGTAGACCTGTGGTCAGAGC	1379
Sbjct	134555	GAAATCCGTGAGTGGATGCCITCTCCCAAGGTGGGGATGGGGGAGACCTGTGGTCAGAGC	134614
Query	1380	CCCCGGGCAGCAGCCACTGCCG--GTCCTTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	1438
Sbjct	134615	CCCCGGGCAGCAGCCACTGC--GAGTCCCTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	134673
Query	1439	CTCCCTGCTGCTCAICCAAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGCTCTTCGC	1498
Sbjct	134674	CTCCATGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGCTCTTCGC	134733
Query	1499	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATGCCACCTGAAGGACCTAGA	1558
Sbjct	134734	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTCTATGCCACCTGAAGGACCTAGA	134793
Query	1559	GGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGA--TCC--AATCCTGGGGC	1615
Sbjct	134794	GGAAGGCATCCAAACGCTGCTGGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCCTGGGGC	134853
Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCAGGC	1675
Sbjct	134854	CCCACTGGCTTCCAGGGACCGGGGAGAGAAACACTGCTGCCCTCTTTTAGTAGTCAGGA	134913
Query	1676	GCTGACCCAAGAGAACTACCGTATTCTTCAATTTCCCTCGTGAATCCTCCAGGCCCTTTC	1735
Sbjct	134914	TCTGACCCAAGAGAACTCATCTTATTTTCATTTCCCTGGCGAATCCTCCAGGCCCTTTC	134973
Query	1736	TCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGAAACAGTGCCC	1795
Sbjct	134974	TCTACAGCCTGGAGGGGAGGGAGGAAAATGAATGAATGAGAGAGGGAGTGAACAGTGCGC	135033
Query	1796	AAGCGCTTGGCCTCTCCTTCTCTTCTTCTTCTTTCAGAGGCTGGAAGATGGCAGCCCCC	1855
Sbjct	135034	AAGCCCTTGGCCTCTCCTTCTCTTCTTCTTCTTTCAGAGGCTGGAAGATGGCAGCCCCC	135093
Query	1856	GGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAAAATCGCACAAACGATG	1915
Sbjct	135094	GGACTGGGTAGATCTTCAAGCAGACCTACAGCAAGTTTGACACAAAATCGCACAAACGATG	135153

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Query 1916   ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG 1975
            |||
Sbjct 135154 ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG 135213

Query 1976   AGACATTCCCTGCGCATCGTGTCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC 2035
            |||
Sbjct 135214 AGACATTCCCTGCGCACCGCTGTCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAACTGC 135273

Query 2036   CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGT-CGTGGAAGGTGCTACT 2094
            |||
Sbjct 135274 CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTTC-TGGAAGGTGCCACT 135332

Query 2095   CCAGTGGCCACCAGCCTTGTCTTAATAAAATAAGTTGCATCATTTTGTGTTGACTAGGTG 2154
            |||
Sbjct 135333 CCAGTGGCCACCAGCCTTGTCTTAATAAAATAAGTTGCATCATTTTGTCTGACTAGGTG 135392

Query 2155   TCCTTGTATAATAATTATGGGGTGGAGGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA 2214
            |||
Sbjct 135393 TCCTTCTATAATAATTATGGAGTGGAGGGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA 135451

Query 2215   GACAACTGTAGGGCCTTCAGGGTCTATTCCGGGAACCAAGGCTGGAGTGCAGTGGCA-G-T 2272
            |||
Sbjct 135452 GACAACTGTAGGGCCTTCAGGGCCTATT-GGGAACCAAGGCTGGAGCGCAGTGGCACGAT 135510

Query 2273   CTGTGCTCGTGCAATCTCCGCCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCG 2332
            |||
Sbjct 135511 CGTGGCTCACTACACCTCCGCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCG 135570

Query 2333   AATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGTGTTAGA 2392
            |||
Sbjct 135571 AATAGTTGGGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGTGTTAGA 135630

Query 2393   GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCAATCTCCTGACCTCAGGTAATCCGCC 2452
            |||
Sbjct 135631 GATGGGGTTTCACCATATTGGCCAGTCTGGTCTCCAATCTCCTGATCTCAGGTAATCCCTCC 135690

Query 2453   CGCCTCGGCCCTCCCAAATTTGCTGGGATTACAGGTATGAGCCACTGGGCCCCTTCCCTGTG- 2511
            |||
Sbjct 135691 CGCCTTGGCCTCCCAAATTTGCTGGGATTACAGGTATGAGGCCACTGGGCCCCTTCCCTGTGCT 135750

Query 2512   CTGTGATTTTTAAAAATAATTATACCAGCAGAAGGACGTCAGACACAGCATGGGCTACCTG 2571
            |||
Sbjct 135751 C-GTGATTTTTAACATAAATTATACCAGCAGGAGGACGTCAGACACAGCATGGGCTACCTG 135809

Query 2572   GCCAIGCCAGCCAGGTTGGACATTTGAGTTGTTTGTCTTGGCACTGTCTCTCATGCAATTG 2631
            |||
Sbjct 135810 GCCGTGCCAGCCGGTTGGACATTTGAGTTGTTTGTCTTGGCACTGTCTCTCATGCGTTG 135869

Query 2632   GGTCCACTCAGTAGATGCTTGTGGAATTC 2660
            |||
Sbjct 135870 GGTCCACTCAGTAGATGCTTGTGGAATTC 135898

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Score = 2963 bits (1604), Expect = 0.0
 Identities = 2075/2294 (90%), Gaps = 65/2294 (2%)
 Strand=Plus/Plus

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Query 1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT 60
            |||
Sbjct 141098 GAATTCAGGAGTGAATGTGCTCAGAACCCCAATCTATTGGCTGTGCT-TTGGCCCCCT 141156

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Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATCGCGGGAGGAGGAAAG	120
Sbjct	141157	TTTCCCAACACACACATTCTGTCTGGTGGCGGAGGTTAAACATCGCGGGAGGAGGAAAG	141216
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGGCCTATCCTGACA	180
Sbjct	141217	GATTAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGG-CTATCCTGACA	141275
Query	181	TCCTTCTCCCGCTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	141276	TCCTTCCCCGCTTCAGGTTGGCCACCATGACCTGCTGCCAGAGGGCACCCACCTGA-CC	141334
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTACAA	300
Sbjct	141335	TTAAAGAGCGGACAAGTTGGGTGGTGTCTCTGGCTGACACTCTGTGCACAACCCCTACAA	141394
Query	301	CGCTGGTATGTTGGGAAGGGAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGTG	360
Sbjct	141395	CGCTGCTGACGTTGGGAAGGGAAGATGACAAGCCAGGAGGATGATCCAGCATGTGTG	141454
Query	361	GGAGGAGCTTCTAAATTATCCATTAGCACAGGCCCGTCAGTGGCCCCAGGCCATAACATG	420
Sbjct	141455	GGAGGAGCTTCTAAATTATCCATTAGCACAGGCCCATCAGTGGCCCCAGGCCATAACGTG	141514
Query	421	CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA--GGTATAAAAAGGGCCCA	479
Sbjct	141515	CAGAGAAACAGGTGGGGAAGCAGCGAGAGAGAAGGGCCAGGGTATAAAAAGGGCCCA	141574
Query	480	CAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGA	539
Sbjct	141575	CAAGAGACCAGCTCCAGGATCCCAAGGCCCAACTCCCCAAACCACTCAGGGTCCTGTGGA	141634
Query	540	CAGCTCA-CTAGCGGCAATGGCTGCAGGTAAAGCGCCCTTAAATCCCTTT--GGCACAATG	597
Sbjct	141635	CAGCTCACCTAGCCGCAAGGCTGCAGGTAAAGCGCCCTTAAATGCCTTTGGGCACAGTG	141694
Query	598	TGTCTGAGGGGAGAGGCGGCGT--CCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	656
Sbjct	141695	TGTCCCAAGGGGAGAAGCGGC--TCCCTGTAGATGGGACGGGGCACTAACCTCAGGTTT	141753
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG--TATTTGGCCAATCTCTGAATG	715
Sbjct	141754	GGGGCTCCTGAATGTGA--ATATCGCCATCGAAGTCCAGATATTTGGCCAATCTCTGAATG	141812
Query	716	TTCTTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAAAAAAACCAGCTCCTGGA	775
Sbjct	141813	TTCTTGGTCCCT--CGGAGG--GA-CG-GAGAGAGAGAAAAAAACA-GCAGCTCCTGGA	141864
Query	776	ACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCT-CTGTTG-CCTCCGGTTTCTCCC	833
Sbjct	141865	ACAGGGAGAGTGTCTGGCTCCTGGTCTCCGGCTCCCTCCT-ITGCCCTCCGGTTTCTCCC	141923
Query	834	CAGGCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAG	893
Sbjct	141924	CAGGCTCCCAGATGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCTGGCTTCAAC	141983
Query	894	AGGGCAG-TGCCCTTCCCAACCATTCCTTATCCAGGCTTTTGGACA-ACG-CTATGCTCC	950
Sbjct	141984	A-GGCTGTGCGGTCCAAACCGTTCCCTTAGCCAGGCTTTTGA-AGA-GACTATGTTCC	142040

Query	951	GCGCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAAGCTCTTG	1008
Sbjct	142041	AAGCCCATCGCGC-GCACACGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGCTCTTG	142098
Query	1009	GGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAA	1067
Sbjct	142099	GGGAATGGGTACGGGTTCAGGGGTGGCAAGAACGGGTGACTTTCCCCCACTGGGGAAGTAA	142158
Query	1068	TGGGAGGAGACTAAGGAGCTCAGGGTTGTTT-TCTGAAGTGAATAATGCAGGCAGATGAGC	1126
Sbjct	142159	TGGGAGGAGACTAAGGAGCTCAGGGTT-TTTATCTGGAGCGAAATGCAGGCAGATGAGC	142217
Query	1127	ATACGCTGAGTGAGGTTCCCGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT----AG-	1181
Sbjct	142218	ATAGGCTGAGCCAGGTTCCCGAAAAGTAACAATGAGAGCTGGTCTCCAGCATAGAAAGC	142277
Query	1182	A-----C--CTT--GG-TGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAG	1231
Sbjct	142278	AGCTTTCTTCTTGGGCGGGGGGGTCTTCTCCTAGGAAGAAGCCTATATCCCAAGGAC	142337
Query	1232	CAGAAGTATTCATTCTCGACAACCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCA	1291
Sbjct	142338	CAGAAGTATTCATTCTCGATCAACCCAGACTTCTCTGCTTCTCAGACTCTATTCCG	142397
Query	1292	ACACCTTCCAAACAGGGTGAAAACGCAGCAGAAATCTGTAGTGGATGCCCTTCTCCCGAGG	1351
Sbjct	142398	ACACCTTCCAAACAGGAAGAAAACAGCAGAAATCCGTAGTGGATGCCCTTCTCCCGAGG	142457
Query	1352	T-GGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGCGACAGCCACTGCCGGTCCCTTC	1410
Sbjct	142458	TGGGGATGGGGGAGACCTGTGGTCAGAGCCCCGGGCGACAGCCACTGTCGGTCCCTTC	142517
Query	1411	CCCTGCAGAACCTAGAGTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGC	1470
Sbjct	142518	CCCTGCAGAACTTAGAGTGCTCCGCATCTCCCTGCGGCTCATGGAGTCGTGGCTGGAGC	142577
Query	1471	CCGTGCAGCTCCTCAGGAGCGTCTTCGCCAACAG-CCTGGTGTATGGCGCTCGGACAGC	1529
Sbjct	142578	CCGTGCGGTTCCTCAGGAGTATCTTACCAAC-GACCTGGTGTATGACACCTCGGACAGC	142636
Query	1530	AACGCTATTCG-CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAG	1588
Sbjct	142637	GATGACTAT-GACCTCTAAAGGACCTAGAAGAAGGCATCCAAACGCTGATGTGGGTGAG	142695
Query	1589	GGTGGCACCA-GGAT--CCAATCTGGGGCCCCACTGGCTTCAGGGACT-GGGGAGAGA	1644
Sbjct	142696	GGTGGCCCCAGGGGTCCCAATCTGGGGCCCCACTGGCTTCAAGG-CTGGGGGAGAGA	142754
Query	1645	AACACTGCTGCCCTCTTTTTCAGAGTCAGGCGCTGACCCAAGAGAATCACCCTATTCTT	1704
Sbjct	142755	AACACTGCTGCCCTCTTTTCAGAGTCAGGCGCTGACCCAAGAGAATCACCCTATTCTT	142814
Query	1705	CATTTCCCTCTGTAATCCTCCAGGCCCTTCTCTACAACTGGAGGGGAGGGAGGAAAAT	1764
Sbjct	142815	CATTTCCCTTGGCGAATCCTCCAGGCCCTTCTCTACAACTGAAAGGGGAGGGAGGAAAAT	142874
Query	1765	GGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCTCTCTCTCTCTCTCTTC	1824
Sbjct	142875	GGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCTCTCTCTCTCTCTCTTC	142934

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Query 1825   ACTTTGCAGAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTAC 1884
            |||
Sbjct 142935 ACTTTGCAGAGGCTGGAAGATGGCAGCCCCAGACTAGGCAGACCCCTAAGCAGACCTAT 142994
            |||

Query 1885   AGCAAGTTTGACACAAAATCGCACACGATGACGCACCTGCTCAAGAACTACGGGCTGCTC 1944
            |||
Sbjct 142995   AACAAAGTTTGACACAAAATCGCACACCATGACGCACCTGCTCAAGAACTACGGGCTGCGC 143054
            |||

Query 1945   TACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGCCGC 2004
            |||
Sbjct 143055   CACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCGCATCGTGCAGTGCCGC 143114
            |||

Query 2005   TCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCA 2064
            |||
Sbjct 143115   TCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCGCGTGGCATCC-TGTGACCCCTCCCA 143173
            |||

Query 2065   GTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCCAGCCTTGTCTTAATAAAA 2124
            |||
Sbjct 143174   GTGCCTCTCCTGCCCCGGGAAGGTGCCACTCCAGTGCCACCCAGCCTTGTCTTAATAAAA 143233
            |||

Query 2125   TTAAGTTGCATCATTTTGTITGACTAGGTGTCCTTGTATAATATTATGGGGTGGAG-GCG 2183
            |||
Sbjct 143234   TAAAGTTGTATCATTTTGTGTGACCAAGGTGTCCTTCTATAATATTATGGGGTGGAAAGTG 143293
            |||

Query 2184   GGTGGTATGGAGCAAGGGGCCAGGTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATT 2243
            |||
Sbjct 143294   G-TGGTATGGAGCAAGGGGCC-AGGT-GGGAAGACGACCTGGAGGGCCTTCAGGGTCTATT 143350
            |||

Query 2244   CGGGAACCAAGGCTG 2257
            |||
Sbjct 143351   -GGGAACTAGGCTG 143363
            |||

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Score = 2817 bits (1525), Expect = 0.0
 Identities = 2052/2297 (89%), Gaps = 74/2297 (3%)
 Strand=Plus/Plus

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Query 1      GAATTCAGCACTGAATC-ATGCCCGAAGCCCCGCAATCTATTGGCTGTGCTTTGGCCCC 59
            |||
Sbjct 156338 GAATTCAGGAGTGAA-CGGTGCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCC 156395
            |||

Query 60     TTTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATCGGGGAGGAGGAAA 119
            |||
Sbjct 156396   TTTTCCCTACACACACATTCTGTCTGGTGGGCGAGGTTCAACATCGGGGAGGAGGAAA 156455
            |||

Query 120    GGAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGGCCTATCTGAC 179
            |||
Sbjct 156456   GGAACAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGG-CTATCTGAC 156514
            |||

Query 180    ATCCTTCTCCGGTTCAGGTGTGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACC 239
            |||
Sbjct 156515   ATCCTTCCCGGCTTCAGGTGTGCCCATCATGGCCTGCTGCCAGAGGGCACCCACCTGACC 156574
            |||

Query 240    CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACA 299
            |||
Sbjct 156575   CTTAAAGAGAGAACGAGTTGGGTGCTGTCTCTGGCTGACACTCTGTGCACAACCCTCACA 156634
            |||

Query 300    ACGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCATGATCCAGCATGTGT 359
            |||

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Sbjct	157520	CGGTCCTTCATGGGGGGGGGGGGCGCATTCTCCTAGGAAGAAGCCTATATTCCA--AAG	157578
Query	1229	GAGCAGAAGTATTCATTCTCTGCA--GAACCCCGACCTCCCTCTGCTTCTCAGAGTCTAT	1287
Sbjct	157579	GAACAGAAGCATTCTCTGTCATGA--CTCCGACACTCC--T--GCTCCTCAGACTCTAT	157634
Query	1288	TCCAACACCTTCCAACAGGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCC	1347
Sbjct	157635	TCCAACACCTTCCAACATGGAGGAAACACAGCAGAAATCCGTGAGTGGATGCCTTCTCCC	157694
Query	1348	CAGGTGGG--ATGGGGTAGACCTGTGGTCAGAGCCCCGGGCGACACAGCCACTGCCGGTC	1406
Sbjct	157695	CAGGCGGGGATGGGGGAGACCTGTGGTCAGAGCCCCGGGCGACACAGCCACTGTCTGGTC	157754
Query	1407	CTTCCCCTGCGAAC--CTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCT	1465
Sbjct	157755	CTTCCCCTGTGAAGACTC--AGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCT	157813
Query	1466	GGAGCCCGTGACAGCTCCTCAGGAGCGTCTTCGCCAAC--AGCCTGGTGTATGGCGCCTCGG	1524
Sbjct	157814	GGAGCCCGTGCGGTTCTCAGGAGTATCTTCGCCAACGA--CCTGGTGTATGACACTCGG	157872
Query	1525	ACAGCAACGCTATCG--CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGG	1583
Sbjct	157873	ACAGCAATGACTAT--GACCTCCTAAAGGACCTAGAAGAAGGCATCCAAACGCTGATGGGG	157931
Query	1584	GTGAGGGTGGCACCAGGA--TCC--AATCTGGGGCCCCACTGGCTTCAGGGAGTGGGG--	1639
Sbjct	157932	GTGAGGGCGGTGCCAGGGGTCCCAATCCTGGAAACCCACTGGCTTGGAGGG--CTGGGGG	157990
Query	1640	AGAGAAACACTGCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAAGAGAATCACCCTTA	1699
Sbjct	157991	AGAGAAACACTGCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAAGAGAATCACCCTTA	158050
Query	1700	TTCTTCATTTCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGG	1759
Sbjct	158051	TTCTTCATTTCCCTGGCGAATCCTCCAGGCCTTTCTCTACACCTGAACGGGAGGGAGG	158110
Query	1760	AAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTT	1819
Sbjct	158111	AAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTT	158170
Query	1820	CCTTCACTTTTGACAGAGGTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGT	1879
Sbjct	158171	CCTTCACTTTTGACAGAGGTGGAAGACGGCAGCCCCAGACTGGGCAGACCTCAAGCAGA	158230
Query	1880	CCTACAGCAAGTTTGACACAAAATCGCACAAACATGACGCACTGCTCAAGAACTACGGGC	1939
Sbjct	158231	CCTACAGCAAGTTTGACACAAAATCGCACAAACATGACGCACTGCTCAAGAACTACGGGC	158290
Query	1940	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCTGCGCATCGTGACAT	1999
Sbjct	158291	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCTGCGCATCGTGACAT	158350
Query	2000	GCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCT	2059
Sbjct	158351	GCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCGGTGGCATCC--TGTGACCCCT	158409
Query	2060	CCCCAGTGCCTCTCTGGTCGTGGAAGGTGCTACTCCAGTGCCCAACGACCTTGTCTCTAA	2119

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Sbjct 158410 CCCCAGTGCCTTTCTCTGGCCCCGGAAGGTGCCACTCCAGTGGCCACCAGCCTTGTCTTAA 158469
Query 2120 TAAAATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCTTGTATAATATTATGGGGTGA 2179
|||||
Sbjct 158470 TAAAATTAAGTTGCATCATTTCTGTCTGACTAGGTGTCTTCTATAATATTATGGGGTGA 158529
Query 2180 G-GCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGT 2238
| |||
Sbjct 158530 AAGTGG-TGGTATGGAGCAAGGGGC-AGGT-GGGAAGACGACCTGTAGGACCTCCGGAT 158586
Query 2239 CTATTCGGGAACCGGC 2255
||||
Sbjct 158587 GTATT-GGGAACTAGGC 158602

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Score = 243 bits (131), Expect = 5e-60
 Identities = 218/259 (84%), Gaps = 10/259 (3%)
 Strand=Plus/Plus

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Query 2250 CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA 2307
|||||
Sbjct 32226 CCAGGCTGGAGTGTCTGTAGAGCAATCTTGGCTCACTGCGACCTCCGCCTCCTGGGTTCAA 32285
Query 2308 GCGATTCTCCTGCCTCAGTCT-CCCAGTATGTTGCGATTCCAGG--CATGCAAGACCA-G 2363
|||||
Sbjct 32286 GCGATTCTCCTACTCTAG-CTTCCGAGTAGCTGGGATTACAGGTGCGTGCCA--CCAGC 32342
Query 2364 GTCAGCTAATTTTTGTATTTTTGGTAGAGACGGGGTTTACCATTATGGCCAGTCTGGT 2423
| |||
Sbjct 32343 GG-CAGCTAATTTTTGTATTTTTATTAGAGACGGGGTTTACCATTATGGCCAGGCTGGT 32401
Query 2424 CTCACCTCTCTGACCTCAGGTAATCCGCCCGCTCGGCCTCCCAAATTTGCTGGGATTACA 2483
|||
Sbjct 32402 CTCAAACTCCCAATCTCAGGTGATCTGCCACCTCGGCCTCCCAAAGTCTGGGATTATA 32461
Query 2484 GGTATGAGCCACTGGGCC 2502
||
Sbjct 32462 GCGTGAGCCACTGTGCC 32480

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Score = 156 bits (84), Expect = 6e-34
 Identities = 155/189 (82%), Gaps = 5/189 (2%)
 Strand=Plus/Plus

```

Query 2276 GGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCC-GAA 2334
|||||
Sbjct 26789 GGCTCACCAGCACCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAG-CTTCTCTGAG 26847
Query 2335 TAGTTGCGATTCCAGGCATGCAAGACAGGCTCAG-CTAATTTTTGTATTTTTGGTAGAG 2393
|||
Sbjct 26848 TAGCTGGGATTACAGGCATGCGCCACCACAC-CTGGCTAATTTT-GTATTTTGTAGTAGAG 26905
Query 2394 ACGGGGTTTACCATTATTTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCC 2453
|||
Sbjct 26906 ACAGGGTTTCTCATGTTGGTCAGGCTGATCTTGAACCTCCGACCTCAGGTAATCCACCC 26965
Query 2454 GCCTCGGCC 2462
|
Sbjct 26966 ACTTCGGCC 26974

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Score = 143 bits (77), Expect = 5e-30
Identities = 206/265 (77%), Gaps = 21/265 (7%)
Strand=Plus/Minus

Query	2250	CCAGGCTGGAGTGCAGTGGC-AG-TCTTGCGTCGCTGCAATCTCCGCCTCTGGGTTCAA	2307
Sbjct	99767	CCAGGCTGCAGTGCAGTGGCGGATCTCGGCTCACTGAACCTCTGCCTCCGGGTTCAT	99708
Query	2308	GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTCGATTCCAGGCA--TG-CA--A-GAC	2360
Sbjct	99707	CCCATTCTCCTGCCTCAGCTCCC-AAGTGGCTGGGACTACAGGCACCTGCCACCACAAC	99649
Query	2361	CAGGCTCA---GCTAAT-T-T-T-TGTATTTTGGTAGAGACGGGGTTTCACCATATTG	2412
Sbjct	99648	CA-ACATAATTTTTTTGTGTGTGTGTATTTTGGTAGAGACGGGGTTTACCGTGTTA	99590
Query	2413	GCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGGCCCTCCCAAATTG	2472
Sbjct	99589	GCCAGGATGGTCTCAATCTCCTGACCTCATG-A-TCCGCCTGCCTTGGACTCCCAAGATG	99532
Query	2473	CTGGGATTACAGGTATGAGCCACTG	2497
Sbjct	99531	CTGGGATTACAGGCGTGAAGCCACTG	99507

>emb|CT954302.6| N.leucogenys DNA sequence from clone CH271-262E11, complete sequence
Length=195471

Score = 3402 bits (1842), Expect = 0.0
Identities = 2117/2248 (94%), Gaps = 25/2248 (1%)
Strand=Plus/Minus

Query	432	GTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCCCACAGAGACCAG	490
Sbjct	74925	GTGGGGAGAAGCAGCGAGAGAGAAGGGGCCAGGGCAATAAAACGGCCCCACAGAGACCAG	74866
Query	491	CTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCA-CTA	549
Sbjct	74865	CTCCAGGATCCCAAGGCCCAACTCCCCAAACCACTCAGGGTCTGTGGACAGCTCACCTA	74806
Query	550	GCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCCTTT-GGCACAATGTGTCTGAGGG	608
Sbjct	74805	GCTGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCCTTTGGGCGCAATGCGTCCAGAGGA	74746
Query	609	GAGAGGCGGCGTCTCTGTAGATGGGACGGGGGCACTAACCTCAGGTTTGGGGCTTATGAA	668
Sbjct	74745	GAGAGGCGGCGCCTCTGTAGATGGGACGGGCACACTAAACCTCAGGTTTGGGCGTGCTGAA	74686
Query	669	TGTTAGCTATCGCCACTTAAGCCCAAGTATTTGGCCAATCTCTGAATGTTCTGGTCCCTG	728
Sbjct	74685	TGTTAG-TATCTCACTTAAGCCCAAGTATTTGGCCAATCTCTGAATGTTCTGGTCCCTG	74627
Query	729	GA--GGAGGCAGAGAGAGAGAGAGAGAG-----AAAAAAAAAACCCAGCTCTGGAACAGGGAG	783
Sbjct	74626	GAGGGAGGTAGAGAGAGAGAGAGAGAAAAAATAAACAGCCCCAGGAGCAGGGAG	74567
Query	784	AGCGCTGGCCTCTGTGCTCCAGCTCCCTCTGIT- GCCTCCGGTTTCTCCCAGGCTCCC	842
Sbjct	74566	AGCGCTGGACTCTGTGCTCCAGCTCCCTCTGTTACCTTCGGTTTCTCCCAGGCTCCC	74507

Query	843	GGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAGAGGGCAGTG	902
Sbjct	74506	GGACGTCCTGCTCCTGGCCTTTGCCCCTGCTCTGCCTGCCTGGCTTCAAGAGGGCAGTG	74447
Query	903	CCTTCCCAACCAATCCCTTATCCAGGCTTTTGGACAACGCTATGCTCCGCGCCCGTCGCC	962
Sbjct	74446	CCTTCCCAACCAATCCCTTATCCAGGCTTTTGGACAATGCTATGCTCCGCGCCCATCGCC	74387
Query	963	TGTACCAAGCTGGCATAATGACACCTATCAGGAGTTTGTAAAGCTC-TTGGGTAAATGGGTGCG	1021
Sbjct	74386	TGGACCAAGCTGGCATTGACACCTACCAGGAGCTTGTAAAGCTCTTTGGG-AATGGGTACG	74328
Query	1022	CTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATGGGAGGAGACTA	1080
Sbjct	74327	CTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGGAAGTAATGGGAGGAGACTA	74268
Query	1081	AGGAGCTCAGGGTGTGTTTTCTGAAGTGAAATGCAGGCAGATGAGCATACGCTGAGTGAG	1140
Sbjct	74267	AGGAGCTCAGGGTGTGTTTTCTGAAGTGAAATGCAGGCAGATGAGCATACGCTGAGTGAG	74208
Query	1141	GTTCGCAAGAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTCTCT	1200
Sbjct	74207	GTTCGCAAGAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGTCTCT	74148
Query	1201	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCTTCTGCAGAACCCCCA	1260
Sbjct	74147	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCTTCTGCAGAACCCCCA	74088
Query	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAACGCAGCA	1320
Sbjct	74087	GACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAACGCAGCA	74028
Query	1321	GAAATCTGTGAGTGGATGCCTTCTCCCCAGGT-GGGAATGGGGTAGACCTGTGGTCAGAGC	1379
Sbjct	74027	GAAATCCGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGGGGAGACCTGTGGTCAGAGC	73968
Query	1380	CCCCGGGCAGCACAGCCACTGCCG-GTCCCTTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	1438
Sbjct	73967	CCCCGGGCAGCACAGCCACTG-CGAGTCCCTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	73909
Query	1439	CTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGC	1498
Sbjct	73908	CTCCATGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGTCTCCTCAGGAGCGTCTTCGC	73849
Query	1499	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAGA	1558
Sbjct	73848	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCACCACCTAAGGAGCTAGA	73789
Query	1559	GGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGCGACCA-GGAT--CCAATCTGGGGC	1615
Sbjct	73788	GGAAGGCATCCAAACGCTGCTGGGGGTGAGGGTGCGCCAGGGGTCCCCAATCTGGGGC	73729
Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTCAGAGTCAGGC	1675
Sbjct	73728	CCCACTGGCTTCCAGGGACCGGGGAGAGAAACACTGCTGCCCTCTTTTTCAGAGTCAGGA	73669
Query	1676	GCTGACCCAAGAGAAGCTACCGTATTCTTCTTCTTCCCTCGTGAACTCTCCAGGCCTTTC	1735
Sbjct	73668	TCTGACCCAAGAGAAGCTATCTTATTCTTCTTCTTCCCTGGCGAATCTCCAGGCCTTTC	73609

Query	1736	TCTACAACCTGGAGGGGAGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTGGCC	1795
Sbjct	73608	TCTACAGCCTGGAGGGGAGGAGGAAAAATGAATGAATGAGAGAGGGAGTGAACAGTGGCG	73549
Query	1796	AAGCGCTTGGCCTCTCCTTCTCTTCTTCTTCTTTCAGAGGCTGGAAGATGGCAGCCCC	1855
Sbjct	73548	AAGCCCTTGGCCTCTCCTTCTCTTCTTCTTCTTTCAGAGGCTGGAAGATGGCAGCCCC	73489
Query	1856	GGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTTTGACACAAAAATCGCACAAACGATG	1915
Sbjct	73488	GGACTGGGTAGATCTTCAAGCAGACCTACAGCAAGTTTGACACAAATCGCACAAACGATG	73429
Query	1916	ACGCACTGCTCAAGAAGTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG	1975
Sbjct	73428	ACGCACTGCTCAAGAAGTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG	73369
Query	1976	AGACATTCCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	2035
Sbjct	73368	AGACATTCCTGCGCACCCTGTCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAAGTGC	73309
Query	2036	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGTTCGTTGGAAGGTGCTACT	2094
Sbjct	73308	CCTGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGTTCGTTGGAAGGTGCTACT	73250
Query	2095	CCAGTGCCCAACGAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTAGTAGGTG	2154
Sbjct	73249	CCAGTGCCCAACGAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTAGTAGGTG	73190
Query	2155	TCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA	2214
Sbjct	73189	TCCTTGTATAATATTATGGAGTGGAGGGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA	73131
Query	2215	GACAACCTGTAGGGCCTTCAGGGTCTATTTCGGAACCAAGGCTGGAGTGCAGTGGCA-G-T	2272
Sbjct	73130	GAGACCTGTAGGGCCTGCGGGTCTATT-GGGAACCAAGGCTGGAGCGAGTGGCAGCAT	73072
Query	2273	CTTGGCTCGCTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCCTGCTCAGTCTCCCG	2332
Sbjct	73071	CGTGGCTCACTACAACCTCTGTCTCCTGGGTTCAAGCGATTCTCCTGCTCAGTCTCCCG	73012
Query	2333	AATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTTGTGATAGA	2392
Sbjct	73011	AATAGTTGGGATTCCAGGCATGCACACCAGGCTCAGCTAATTTTGTATTTTGTGATAGA	72952
Query	2393	GACGGGGTTTACCACATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC	2452
Sbjct	72951	GACGGGGTTTACCACATATTGGCCAGTCTGGTCTCCATCTCCTGATCTCAGGTAATCTCC	72892
Query	2453	CGCCTCGGCCCTCCAAATTGCTGGGATTACAGGTATGAGGCACTGGGCCCTTCCTGTCC	2512
Sbjct	72891	CGCCTTGGCCCTCCAAATTGCTGGGATTACAGGTAGGAGCACTGGGCCCTTCCTGTCT	72832
Query	2513	TGTGATTTTAAAAATAATTATACAGCAGAGGACGTCCAGACACAGCATGGGCTACCTGG	2572
Sbjct	72831	TGTGATTTTAAACATAATTATACAGCAGGAGGACGTCCAGACACAGCATGGGCTACCTGG	72772
Query	2573	CCATGCCAGCCAGTGTGGACATTTGAGTTGTTTGGCTTGGCAGTGTCTCTCATGCTATGG	2632
Sbjct	72771	CCATGCCAGCTGGTGTGGACATTTGAGTTGTTTGGCTTGGCAGTGTCTCTCATGCTATGG	72712

Query 2633 GTCCACTCAGTAGATGCTTGTGTAATTC 2660
 |||
 Sbjct 72711 GTCCACTCAGTAGATGCTTGTGTAATTC 72684

Score = 2913 bits (1577), Expect = 0.0
 Identities = 2067/2295 (90%), Gaps = 67/2295 (2%)
 Strand=Plus/Minus

Query 1 GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60
 |||
 Sbjct 67457 GAATTCAGGAGTGAATGGTGCTCAGAACCCCAACAATCTATTGGCTGTGC-TTGGCCCT 67399

Query 61 TTTCCTCAACACACACATTCTGCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
 |||
 Sbjct 67398 TTTCCTCAACACACACATTCTGCTGGTGGGCGGAGGTTAAACATGCGGGGAGGAGGAAAG 67339

Query 121 GAATAGGATAGAGAGTGGGATGGGTCCGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
 |||
 Sbjct 67338 GATTAGGATAGAGAGTGGGATGGGTCCGTAGGGGTCTCAAGGACTGG-CTATCCTGACA 67280

Query 181 TCCTTCTCCGCGTTCAGGTTGGCCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC 240
 |||
 Sbjct 67279 TCCTTCCCCGCGTTCAGGTTGGCCACCATGACCTGCTGCCAGAGGGCACCCACCTGA-CC 67221

Query 241 TTAAGAGAGGACAAAGTTGGGTGGTATCTCTGGCTGACATTCCTGTGCACACCCCTCACA 300
 |||
 Sbjct 67220 TTAAGAGCGGACAAAGTTGGGTGGTGTCTCTGGCTGACACTCTGTGCGCAACCCCTCACA 67161

Query 301 CGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGCGATGATCCAGCATGTGTG 360
 |||
 Sbjct 67160 CGCTGCTCACGGTGGGAAGGAAAGATGACAGGCCAGGAGGCATGATCCAGCATGTGTG 67101

Query 361 GGAGGAGCTTCTAAATTAATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCCTAAACATG 420
 |||
 Sbjct 67100 GGAGGAGCTTCTGAATTATCCATTAGCACAAAGCCCATCAGTGGCCCCAGGCCCTAAACGTG 67041

Query 421 CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAGGGGCCA 479
 |||
 Sbjct 67040 CAGAGAAACAGGTGGGAGAAGCAGCGAGAGAGAAGGGGCCAGGGTATAAAAGGGGCCG 66981

Query 480 CAAGAGACCAGCTCAAGGATCCCAAGGCCCACTCCCCGAACCACTCAGGGTCTCTGTGGA 539
 |||
 Sbjct 66980 CAAGAGACCAGCTCCAGGATCCCAAGGCCCACTCCCCAACCCTCAGGGTCTCTGTGGA 66921

Query 540 CAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTT-GGCACAATG 597
 |||
 Sbjct 66920 CAGCTCACTAGCGGCAAGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGGACAGATG 66861

Query 598 TGICCTGAGGGGAGAGGCGGCGT-CCCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT 656
 |||
 Sbjct 66860 TGTCCTAAGGGGAGAGGCGGC-TCCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT 66802

Query 657 GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAAG-TATTGGCCAATCTCTGAATG 715
 |||
 Sbjct 66801 GGGGCTCCTGAATGTGA-ATATCGCCATCGAAGTCCAGATATTGGCCAATCTCTGAATG 66743

Query 716 TTCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775
 |||


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Sbjct  65860  GGGTGGCCCCAGGGGTCCCCAATCCTGGGGCCCCACTGGCTTCAAGGG-CTGGGGGAGAG 65802
Query  1644    AAACACTGCTGCCCTCTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGGTATTCT 1703
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65801    AAACACTGCTGCCCTCTTTCTAGCAGTCAGGCACTGACCCAAGAGAACTACCTTATTCT 65742
Query  1704    TCATTTCCCTCGTGAATCCTCCAGGCCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAA 1763
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65741    TCATTTCCCTGGCGAATCCTCCAGGCCCTTTCTCTACACCTGAAGGGGAGGGAGGAAAA 65682
Query  1764    TGGATGAATGAGAGAGGGAGGGAACAGTGCCTTGGGCTCTCCTTCTCTTCTCT 1823
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65681    TGGATGAATGAGAGAGCGAGGGAACAGTGCCTTGGGCTCTCCTTCTCTTCTCT 65622
Query  1824    CACTTTGCAGAGGCTGGAAGATGGCAGCCCCGGGACTGGGCAGATCTTCAATCAGTCTTA 1883
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65621    CACTTTGCAGAGGCTGGAAGAGCGCAGCCCCAGACTGGGCAGACCTCAAGCAGACCTA 65562
Query  1884    CAGCAAGTTTGACACAAAATCGCACACGATGACGCAGCTGCTCAAGAACTACGGGCTGCT 1943
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65561    TAACAAGTTTGACACAAAATCGCACACCAATAACGCAGCTGCTCAAGAACTACGGGCTGCG 65502
Query  1944    CTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCATCTGTCAGTGCCG 2003
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65501    CCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTCGCATCTGTCAGTGCCG 65442
Query  2004    CTCGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCC 2063
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65441    CTCGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCGGTGGCATCC-TGTGACCCCTCCCC 65383
Query  2064    AGTGCTCTCCTGGTCTGGAAGGTGCTACTCCAGTGGCCACCAGCCTTGTCTTAATAAA 2123
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65382    AGTGCTCTCCTGGCCCGGAAGGTGCTCCAGTGGCCACCAGCTTGTCTTAATAAA 65323
Query  2124    ATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAG-GC 2182
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65322    ATAAAGTTGTATCATTTTGTCTGACCAGGTGTCCTTCTATAATATTATGGGGTGGAAAGT 65263
Query  2183    GGGTGGTATGAGGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTACGGGTCTAT 2242
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  65262    GG-TGGTATGAGGCAAGGGGC-AGGT-GGGAAGACGACCTGGAGGGCCTTACGGGTCTAT 65206
Query  2243    TCGGGAACAGGCTG 2257
          |||||  |||||
Sbjct  65205    T-GGGAACAGGCTG 65192

```

Score = 2832 bits (1533), Expect = 0.0
 Identities = 2054/2296 (89%), Gaps = 73/2296 (3%)
 Strand=Plus/Minus

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Query  1      GAATTCAGCACTGAATC-ATGCCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCC 59
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  52167    GAATTCAGGAGTGAA-CGGTGTCTCAGAACCCCAATCTATTGGCTGTGC-TTGGCCCC 52110
Query  60      TTTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAA 119
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct  52109    TTTTCCCTACACACACATTCTGTCTGGTGGGCGGAGGTTCACATGCGGGGAGGAGGAAA 52050
Query  120     GGAATAGGATAGAGAGTGGGAATGGGCTCGGTAGGGGTCTCAAGGACTGGCCTATCTGAC 179

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3/2/09

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      | |||||
Sbjct 181609 ACTTCGGCC 181601

Score = 148 bits (80), Expect = 1e-31
Identities = 207/265 (78%), Gaps = 21/265 (7%)
Strand=Plus/Plus

Query 2250 CCAGGCTGGAGTGCAGTGGC-AG-TCTTGGCTCGCTGCAATCTCCGCTCCTGGGTCAA 2307
          |||||
Sbjct 108830 CCAGGCTGCAGTGCAGTGGCGCATCTCGGCTCAGTAAACCTCTGCTCCCGGTTTCAT 108889

Query 2308 GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TG-CA--A-GAC 2360
          |||||
Sbjct 108890 CCCATTCTCCTGCCTCAGCTCCC-AAGTGGCTGGGACTACAGGCACCTGCCACCAAC 108948

Query 2361 CAGGCTCA----GCTAAT-T-T-T-TGTATTTTGGTAGAGACGGGGTTTCACCATATTG 2412
          |||||
Sbjct 108949 CA-ACTAATTTTTTTTGTGTGTGTAATTTTGGTAGAGACGGGGTTTCACCGTGTTA 109007

Query 2413 GCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCTCGGCCTCCCAATTG 2472
          |||||
Sbjct 109008 GCCAGGATGGTCTCAATCTCCTGACCTCATG-A-TCCGCTGCCTTGGCTCCAGAGTG 109065

Query 2473 CTGGGATTACAGGTATGAGCCACTG 2497
          |||||
Sbjct 109066 CTGGGATTACAGGCGTGAGCCACTG 109090

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>gb|EU421712.1| Homo sapiens growth hormone 1 (GH1) gene, complete cds, alternative
spliced
Length=2212

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Score = 3254 bits (1762), Expect = 0.0
Identities = 2084/2235 (93%), Gaps = 39/2235 (1%)
Strand=Plus/Plus

Query 106 CGGGGAGGAGGAAAGGAATAGGATAGAGAGTGGGATGGGGTCGGTA-GGGGTCTCAAGGA 164
          |||||
Sbjct 1 CGGGGAGGAGGAAAGGATAGGATAGAGAAATGGGATGTGGTTCGGTAGGGGGTCTCAAGGA 60

Query 165 CTGGCTATCCTGACATCCTTCTCCGCTTCAGGTTGGCCACCATGGCCTGCTGCCAGAG 224
          |||||
Sbjct 61 CTGG-CTATCCTGACATCCTTCTCCGCTGTCAGGTTGGCCACCATGGCCTGCTGCCAGAG 119

Query 225 GGCACCCACGTGACCCCTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCG 284
          |||||
Sbjct 120 GGCACCCACGTGACCCCTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACACTCG 179

Query 285 TGCACAACCCCTCACAACGCTGGTGATGGTGGGAAGGAAAGATGACAAGTCAGGGGGCAT 344
          |||||
Sbjct 180 TGCACAACCCCTCACAACACTGGTGACGGTGGGAAGGAAAGATGACAAGCCAGGGGGCAT 239

Query 345 GATCCCAGCATGTGTGGGAGGAGCTTCTAAATTATCATTAGCACAAAGCCCGTCAGTGGC 404
          |||||
Sbjct 240 GATCCCAGCATGTGTGGGAGGAGCTTCTAAATTATCATTAGCACAAAGCCCGTCAGTGGC 299

Query 405 CCCAGGCCTAAATGCAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAGGGGCCA- 462
          |||||
Sbjct 300 CCCATGCATAAATGTACACAGAAACAGGTG-GGGGCAA-CAGTGGGAGAGAGGGGCCAG 357

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Query	463	GGTATAAAAAGGGCCACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACC	522
Sbjct	358	GGTATAAAAAGGGCCACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACC	417
Query	523	ACTCAGGGTCTGTGGACAGCTCA-CTAGCGCAATGGCTGCAGGTAAGCGCCCTAAAA	581
Sbjct	418	ACTCAGGGTCTGTGTGGACAGCTCAGCTAGCTGCAATGGCTACAGGTAAGCGCCCTAAAA	477
Query	582	TCCCTTTT-GGCACAATGTGTCTGAGGGGAGAGGCGGCTCTGTAGTAGGGACGGGGG	640
Sbjct	478	TCCCTTTTGGGCACAATGTGTCTGAGGGGAGAGGACGACCTGTAGTAGGGACGGGGG	537
Query	641	ACTAACCCCTCAGGTTTGGGGCTTATGAATGTTAGCTATCGCATCTAAGCCAGTATTG	700
Sbjct	538	ACTAACCCCTCAGGTTTGGGGCTTCTGAATGTGAG-TATGCCATGTAGCCAGTATTG	596
Query	701	GCCAATCTCTGAATGTTCTCTGGTCCCTGGAGGAGGAGAGAGAGAGAGAAAAAAA	760
Sbjct	597	GCCAATCTCAGAAAGCTCTCTGGTCCCT---GGA-G--G-GA-TG-GAGAGAG-AAAAACA	646
Query	761	AACCAGCTCTCGGAACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-C	819
Sbjct	647	AA--CAGCTCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGCTCCCTCTGTTGCC	704
Query	820	CTCCGGTTTCTCCCGAGGCTCCCGGACGTCCTGCTCTGCTGCTTTTGGCTGCTCTGCCT	879
Sbjct	705	CTCTGGTTTCTCCCGAGGCTCCCGGACGTCCTGCTCTGCTGCTTTTGGCTGCTCTGCCT	764
Query	880	GTCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAA	939
Sbjct	765	GCCCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAA	824
Query	940	CGCTATGCTCCGCGCCCGTGCCTGTACAGCTGGCATATGACACCTATCAGGAGTTTGT	999
Sbjct	825	CGCTATGCTCCGCGCCCATCGCTGCACAGCTGGCCTTTGACACCTACCAGGAGTTTGT	884
Query	1000	AAGCTCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCGCTG	1059
Sbjct	885	AAGCTCTTGGGAAATGGGTGCGCATCAGGGGTGGCAGGAAGGGGTGACTTTCCCCGCTG	944
Query	1060	GGAAGTAATG-GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGC	1118
Sbjct	945	GGAAATAA-GAGGAGGAGACTAAGGAGCTCAGGGTT-TTCCCGAAGCGAAATGCAGGC	1002
Query	1119	AGATGAGCATACGCTGAGTGAGGTTCCCGAAAAAGTAACAATGGGAGCAGGTCTCCAGCA	1178
Sbjct	1003	AGATGAGCACAGCTGAGTGAGGTTCCCGAAAAAGTAACAATGGGAGCTGGTCTCCAGCG	1062
Query	1179	TAGACCTTGGTGGGCGGTCTCTCTCTAGGAAGAAGCCTATATCTGAAGGAGCAGAAGT	1238
Sbjct	1063	TAGACCTTGGTGGGCGGTCTCTCTCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGT	1122
Query	1239	ATTCATCTCTGCAGAACCCCGAGCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTT	1298
Sbjct	1123	ATTCATCTCTGCAGAACCCCGAGCTCCCTCTGCTTCTCAGAGTCTATTCCGACACCTT	1182
Query	1299	CCAACAGGGTGAAACGAGCAGAAAATCTGTGAGTGGATGCCTTCTCCCGAGG-TGGGAT	1357
Sbjct	1183	CCAACAGGGAGGAAACACAACAGAAATCCGTGAGTGGATGCCTTCTCCCGAGCGGGGAT	1242

Query	1358	GGGGTAGACCTGTGGTCAGAGCCCCGGGAGCAGCAGCCACTGCCGGTCTTCCCTGCA	1417
Sbjct	1243	GGGGGAGACCTGTAGTCAGAGCCCCGGGAGCAGCAGCCAAATGCCCGTCTTCCCTGCA	1302
Query	1418	GAACCTAGAGCTGCTCCGCATCTCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGA	1477
Sbjct	1303	GAACCTAGAGCTGCTCCGCATCTCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGA	1362
Query	1478	GCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGATAGGCGCCTCGGACAGCAACGTCTA	1537
Sbjct	1363	GTTCTCAGGAGTGCTTCGCCAACAGCCTGGTGATAGGCGCCTCTGACAGCAACGTCTA	1422
Query	1538	TCG-CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGTGAGGGTGGCAC	1596
Sbjct	1423	T-GACCTCTCAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGTGAGGGTGGCGC	1481
Query	1597	CA-GGAT--CCATCCTGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGC	1652
Sbjct	1482	CAGGGTGCCCCAATCCTGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGC	1540
Query	1653	TGCCCTCTTTTATGAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTCC	1712
Sbjct	1541	TGCCCTCTTTTATGAGCAGCAGGCGCTGACCCAAGAGAACTCACCTTATTCTTCATTCC	1600
Query	1713	CTCGTGAATCCTCCAGGCGCTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAAT	1772
Sbjct	1601	CTCGTGAATCCTCCAGGCGCTTCTCTACACCTGAAGGGGAGGGAGGAAAATGAATGAAT	1660
Query	1773	GAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCA	1832
Sbjct	1661	GAGAAAGGGAGGGAACAGTACCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCA	1720
Query	1833	GAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCTACAGCAAGTT	1892
Sbjct	1721	GAGGCTGGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTT	1780
Query	1893	TGACACAAAATCGCACACAGTACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTT	1952
Sbjct	1781	CGACACAAACTCACACACAGTACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTT	1840
Query	1953	CAGGAAGGACATGGACAAGGTTCGAGACATTCTGCGCATCGTGAGTCCCGCTCTGTGGA	2012
Sbjct	1841	CAGGAAGGACATGGACAAGGTTCGAGACATTCTGCGCATCGTGAGTCCCGCTCTGTGGA	1900
Query	2013	GGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCT	2072
Sbjct	1901	GGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCT	1960
Query	2073	CCTGGTCTGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGCTCAATAAAATTAAGTTG	2132
Sbjct	1961	CCTGGCCCTGGAAGTTCGCACCTCAGTGCCCAACAGCCTTGCTCAATAAAATTAAGTTG	2020
Query	2133	CATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATG	2192
Sbjct	2021	CATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATG	2080
Query	2193	GAGCAAGGGGCCAGGTGTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACCA	2252
Sbjct	2081	GAGCAAGGGGCCAAG-TTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATT-TGGGAACCA	2138

Query	837	GCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGG	896
Sbjct	659		718
		GCTCCCGGACGTCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGG	
Query	897	GCAGTGCCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACGCTATGCTCCGCGCCC	956
Sbjct	719		778
		GCAGTGCCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACGCTATGCTCCGCGCCC	
Query	957	GTCGCCGTGACCAGCTGGCATAATGACACCTATCAGGAGTTTGAAGCTCTTGGGTAATGG	1016
Sbjct	779		838
		ATCGCCTGACCAGCTGGCATAATGACACCTATCAGGAGTTTGAAGCTCTTGGGTAATGG	
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	839		898
		GTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAAGTAATGGGAGGAG	
Query	1077	ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGACAGGCAGATGAGCATACGCTGAG	1136
Sbjct	899		958
		ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGACAGGCAGATGAGCACACGCTGAG	
Query	1137	TGAGGTTCCCGAGAAAGTAACAATGGGAGCAGGCTCCAGCATAGACCTTGGTGGGCGGT	1196
Sbjct	959		1018
		TGAGGTTCCCGAGAGAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGT	
Query	1197	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAAC	1256
Sbjct	1019		1078
		CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAAC	
Query	1257	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	1316
Sbjct	1079		1138
		CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	
Query	1317	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCGAGGTGGG-ATGGGGTAGACCTGTGGTCA	1375
Sbjct	1139		1198
		AGCAGAAATCCGTGAGTGGATGCCTTCTCCCGAGGTGGGGATGGGGGAGACCTGTGGTCA	
Query	1376	GAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTGCAGAACCTAGAGCTGCTCCG	1435
Sbjct	1199		1258
		GAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCTGCAGAACCTAGAGCTGCTCCG	
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	1495
Sbjct	1259		1318
		CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	
Query	1496	CGCCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGCTTATCGCCACCTGAAGGACCT	1555
Sbjct	1319		1378
		CGCCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGCTTATCGCCACCTGAAGGACCT	
Query	1556	AGAGGAAGGATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC--AATCCTGG	1612
Sbjct	1379		1438
		AGAGGAAGGATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCCCAATCCTGG	
Query	1613	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	1672
Sbjct	1439		1498
		GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	
Query	1673	GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCTCTGTAATCCTCCAGGCCT	1732
Sbjct	1499		1558
		GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCTCTGTAATCCTCCAGGCCT	

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Query 1733 TTCTCTACAACCTGGAGGGGAGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTG 1792
          |||
Sbjct 1559 TTCTCTACAACCTGGAGGGGAGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAACAGTC 1618

Query 1793 CCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCC 1852
          |||
Sbjct 1619 CCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGAGAGGCTGGAAGATGGCAGCC 1678

Query 1853 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 1912
          |||
Sbjct 1679 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 1738

Query 1913 ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG 1972
          |||
Sbjct 1739 ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG 1798

Query 1973 TCGAGACATTCTCGGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 2032
          |||
Sbjct 1799 TCGAGACATTCTCGGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 1858

Query 2033 TGCCCGGGTGGGCATCCCTGIGA 2054
          |||
Sbjct 1859 TGCCCGGGTGGGCATCCCTGIGA 1879

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Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Mar 1, 2009 5:49 PM

Number of letters in database: 660,889,664

Number of sequences in database: 8,293,739

```

Lambda      K      H
1.33      0.621    1.12
Gapped
Lambda      K      H
1.28      0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 8293739
Number of Hits to DB: 7398931
Number of extensions: 2386
Number of successful extensions: 2386
Number of sequences better than 10: 1140
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 2296
Number of HSP's successfully gapped: 2295
Length of query: 2660
Length of database: 26430693440
Length adjustment: 34
Effective length of query: 2626
Effective length of database: 26148706314
Effective search space: 68666502780564
Effective search space used: 68666502780564
A: 0
X1: 15 (28.8 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 15 (28.8 bits)

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S2: 23 (43.6 bits)